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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:42:01 ; Search time 166 Seconds
(without alignments)
135.133 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329
Sequence: 1 YPVRCILPPATGPGKARIIR.....RGNNANPASEQECSSCGGS 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	58	6	ABG71914 Human Kun
2	326	99.1	58	6	ABG71915 Human Kun
3	314	95.4	58	6	ABG71917 Human Kun
4	314	95.4	111	6	ABG71920 Human 212
5	291	88.4	58	6	ABG71916 Human Kun
6	291	88.4	111	6	ABG71919 Human 212
7	264	80.2	58	4	ABAB60623 Human K12
8	264	80.2	58	6	ABG71912 Human Kun
9	264	80.2	58	6	ADL16831 Human BTL
10	264	80.2	111	6	ABG71918 Human HKT
11	264	80.2	189	4	AAAB60634 Human pro
12	264	80.2	189	8	ADL16845 Human pro
13	264	80.2	1235	8	ADOS5146 Protein #
14	264	80.2	1280	6	ABR58408 Human NOV
15	220.5	67.0	51	4	AAAB60631 Human pro
16	220.5	67.0	51	8	ADL16839 Human pro
17	208	63.2	109	2	AAAR22985 Human ty
18	203	61.7	111	2	AAAR22988 Human ty
19	202	61.4	109	2	AAAR22983 Human ty
20	202	61.4	128	2	AAAR22983 Human ty
21	199	60.5	57	2	AAAM47433 Human ty
22	198	60.5	141	2	AAAR22982 Human ty
23	195	59.3	128	2	AAAR22982 Human ty
24	194	59.0	111	2	AAAR22980 Human ty
25	194	59.0	128	2	AAAR22980 Human ty

26	194	59.0	141	2	AAAR22988 Human ty
27	194	59.0	141	2	AAAR22986 Human ty
28	193	58.7	56	1	AAAP3399 Human ty
29	193	58.7	57	2	AAAM47436 Human ty
30	193	58.7	57	2	AAAM47434 Human ty
31	193	58.7	57	2	AAAM47432 Human ty
32	193	58.7	57	2	AAAM47435 Human ty
33	193	58.7	128	2	AAAR22981 Human ty
34	193	58.7	128	2	AAAR22981 Human ty
35	193	58.7	141	2	AAAR22984 Human ty
36	193	58.7	141	2	AAAR22984 Human ty
37	192	58.4	58	1	AAAP33401 Human ty
38	192	58.4	58	2	AAAR27373 Human ty
39	192	58.4	58	2	AAAR47179 Human ty
40	192	58.4	58	2	AAAR78426 Human ty
41	192	58.4	58	2	AAAR81885 Human ty
42	192	58.4	58	2	AAAP9147 Human ty
43	192	58.4	58	2	AAAM64119 Human ty
44	192	58.4	58	2	AAAM66410 Human ty
45	192	58.4	58	2	AAAM79983 Human ty

ALIGNMENTS

RESULT 1	ABG71914	standard; protein; 58 AA.
ID	ABG71914	
XX	ABG71914	
AC	ABG71914	
DT	22-JAN-2003	(first entry)
XX		
DE	Human Kunitz protease inhibitor protein HKI-18, mutant #1.	
XX		
KW	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;	
KW	anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;	
KW	systemic inflammatory response syndrome; acute pancreatitis;	
KW	shock syndrome; disseminated intravascular coagulation; mutant;	
KW	hyperfibrinolytic haemorrhage; myocardial infarction; mutant;	
KW	cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;	
KW	allergy-induced protease release; deep vein thrombosis;	
KW	adult respiratory distress syndrome; chronic inflammatory bowel disease.	
OS	Homo sapiens.	
XX		
XX	Synthetic.	
OS		
FH	Key	Location/Qualifiers
FT	Misc-difference 9	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 11	/note= "Wild-type His substituted by Thr"
FT	Misc-difference 13	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 15	/note= "Wild-type Ala-Asp-Trp-Ala-Ala substituted by Lys-Ala-Arg-Ile-Ile"
FT	Misc-difference 34	/note= "Wild-type Trp substituted by Val"
FT	Misc-difference 39	/note= "Wild-type His substituted by Arg"
XX		
XX	W0200296938-A2.	
XX		
PD	05-DEC-2002.	
XX		
XX	31-MAY-2002; 2002MO-DK000372.	
PF		
XX		
XX	31-MAY-2001; 2001DK-00000859.	
PR		
XX	05-JUL-2001; 2001US-0303180P.	
XX		
XX	(NOVO) NOVO NORDISK AS.	
PA		
XX		

BEST AVAILABLE COPY

PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
 XX MPI; 2003-041403/03.
 XX Kunitz-type protease inhibitor used in the treatment of inflammatory
 PT disorders.
 XX Claim 20; Page 49; 52pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising a 51 amino
 CC acid sequence being a generic sequence for a Kunitz-type protease
 CC inhibitor or a variant where the sequence is at least 80% identical to
 CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 CC included are an isolated polypeptide obtainable by cultivation of a host
 CC cell comprising a polynucleotide construct encoding kunitz-type protein
 CC in an appropriate growth medium under conditions allowing expression of
 CC the polynucleotide construct and recovering the polypeptide from the
 CC culture medium; a polynucleotide construct encoding the kunitz-type
 CC protein and a host cell comprising the polynucleotide construct. The
 CC kunitz-type protein is used for the preparation of a medicament for the
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 CC haemorrhage, myocardial infarction, for prevention of blood loss during
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 CC allergy-induced protease release; deep vein thrombosis, emphysema,
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
 CC inflammatory bowel disease, and psoriasis. The present sequence is a
 CC human HKI-18 mutant sequence
 XX
 SQ Sequence 58 AA;
 Query Match 100.0%; Score 329; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.1e-31;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YPVRCLLPATGPKCARIRIRWFVAVSGGCRNFVYGGCRGNANNNFASBEGCMSSCGQS 58
 DB 1 YPVRCLLPATGPKCARIRIRWFVAVSGGCRNFVYGGCRGNANNNFASBEGCMSSCGQS 58
 RESULT 2
 ABG71915
 ID ABG71915 standard; protein; 58 AA.
 AC ABG71915;
 XX
 XX 22-JAN-2003 (first entry)
 DT
 XX Human Kunitz protease inhibitor protein HKI-18, mutant #2.
 DE
 XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
 KW anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation; mutant;
 KW hyperfibrinolytic haemorrhage; myocardial infarction; muten;
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
 KW allergy-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 9 /note= "Wild-type Ser substituted by Pro"
 FT MISC-difference 11 /note= "Wild-type His substituted by Thr"
 FT MISC-difference 13 /note= "Wild-type Ser substituted by Pro"
 FT MISC-difference 15..19 /note= "Wild-type Ala-Asp-Trip-Ala-Ala substituted by Arg-
 FT Ala-Arg-Ile-Ile"
 FT MISC-difference 34

FT /note= "Wild-type Trp substituted by Val"
 FT MISC-difference 39 /note= "Wild-type His substituted by Arg"
 FT
 XX
 XX MO200296938-A2.
 XX
 XX 05-DEC-2002.
 PD
 XX
 XX 31-MAY-2002; 2002WO-DK000372.
 PF
 XX 31-MAY-2001; 2001DK-00000859.
 PR 05-JUL-2001; 2001US-0303180P.
 XX
 XX (NOVO) NOVO NORDISK AS.
 PA
 XX Jorgensen MU, Bang S, Olsen OH, Petersen LC;
 PI MPI; 2003-041403/03.
 DR
 XX Kunitz-type protease inhibitor used in the treatment of inflammatory
 PT disorders.
 XX Claim 20; Page 49; 52pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising a 51 amino
 CC acid sequence being a generic sequence for a Kunitz-type protease
 CC inhibitor or a variant where the sequence is at least 80% identical to
 CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 CC included are an isolated polypeptide obtainable by cultivation of a host
 CC cell comprising a polynucleotide construct encoding kunitz-type protein
 CC in an appropriate growth medium under conditions allowing expression of
 CC the polynucleotide construct and recovering the polypeptide from the
 CC culture medium; a polynucleotide construct encoding the kunitz-type
 CC protein and a host cell comprising the polynucleotide construct. The
 CC kunitz-type protein is used for the preparation of a medicament for the
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 CC haemorrhage, myocardial infarction, for prevention of blood loss during
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 CC allergy-induced protease release; deep vein thrombosis, emphysema,
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
 CC inflammatory bowel disease, and psoriasis. The present sequence is a
 CC human HKI-18 mutant sequence
 CC
 XX
 SQ Sequence 58 AA;
 Query Match 99.1%; Score 326; DB 6; Length 58;
 Best Local Similarity 98.3%; Pred. No. 2.4e-31;
 Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YPVRCLLPATGPKCARIRIRWFVAVSGGCRNFVYGGCRGNANNNFASBEGCMSSCGQS 58
 DB 1 YPVRCLLPATGPKCARIRIRWFVAVSGGCRNFVYGGCRGNANNNFASBEGCMSSCGQS 58
 RESULT 3
 ABG71917
 ID ABG71917 standard; protein; 58 AA.
 AC ABG71917;
 XX
 XX 22-JAN-2003 (first entry)
 DT
 XX Human Kunitz protease inhibitor protein HKI-18, mutant #4.
 DE
 XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
 KW anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation; mutant;
 KW hyperfibrinolytic haemorrhage; myocardial infarction; muten;
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
 KW allergy-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.

```

XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT MISC-difference 9 /note= "Wild-type Ser substituted by Pro"
FT MISC-difference 11 /note= "Wild-type His substituted by Thr"
FT MISC-difference 13 /note= "Wild-type Ser substituted by Pro"
FT MISC-difference 15.17 /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
FT MISC-difference 34 /note= "Wild-type Trp substituted by Val"
XX PN W0200296938-A2.
XX PD 05-DEC-2002.
XX PF 31-MAY-2002; 2002WO-DK000372.
XX PR 31-MAY-2001; 2001DK-00000859.
XX PR 05-JUL-2001; 2001US-0303180P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
XX DR WPI; 2003-041403/03.
XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
XX PT disorders.
XX PS Claim 20; Page 49; 52pp; English.
XX XX The invention relates to an isolated polypeptide comprising a 51 amino
XX CC acid sequence being a generic sequence for a Kunitz-type protease
XX CC inhibitor or a variant where the sequence is at least 80% identical to
XX CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
XX CC included are an isolated polypeptide obtainable by cultivation of a host
XX CC cell comprising a polynucleotide construct encoding kunitz-type protein
XX CC in an appropriate growth medium under conditions allowing expression of
XX CC the polynucleotide construct and recovering the polypeptide from the
XX CC culture medium, a polynucleotide construct encoding the kunitz-type
XX CC protein and a host cell comprising the polynucleotide construct. The
XX CC kunitz-type protein is used for the preparation of a medicament for the
XX CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
XX CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
XX CC haemorrhage, myocardial infarction, for prevention of blood loss during
XX CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, emphysema,
XX CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
XX CC inflammatory bowel disease, and psoriasis. The present sequence is a
XX CC human HKI-18 mutant sequence
XX SQ Sequence 58 AA;
XX Query Match 95.4%; Score 314; DB 6; Length 58;
XX Best Local Similarity 94.8%; Pred. No. 6.6e-30;
XX Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 YPVACLPATGPGKARIIRYFVASVGQGNRFYGGCGRGNANNPASBOECMSQGS 58
Db 1 YPVACLPATGPGKARIRYFVASVGQGNRFYGGCGRGNANNPASBOECMSQGS 58

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DT 22-JAN-2003 (first entry)
XX DE Human 212L-HKI-18-2 fusion protein.
XX XX
XX KM Human, protease inhibitor, kunitz; HKI-18; antiinflammatory; mutant;
XX KM anticoagulant; coagulant; cardiac; CPB; psoriasis; emphysema; mutein;
XX KM systemic inflammatory response syndrome; acute pancreatitis;
XX KM shock syndrome; disseminated intravascular coagulation; yeast;
XX KM hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
XX KM cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
XX KM allergy-induced protease release; deep vein thrombosis;
XX KM adult respiratory distress syndrome; chronic inflammatory bowel disease.
XX OS Homo sapiens.
XX OS Saccharomyces cerevisiae.
XX OS Synthetic.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT Peptide 1..51
XX FT /label= 212L_signal_peptide
XX FT Cleavage-site 52..53
XX FT /label= KEX2_cleavage_site
XX FT Protein 54..111
XX FT /label= HKI_18
XX FT MISC-difference 62 /note= "Wild-type Ser substituted by Pro"
XX FT MISC-difference 64 /note= "Wild-type His substituted by Thr"
XX FT MISC-difference 68..70 /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
XX FT /note= "Wild-type Trp substituted by Val"
XX PN W0200296938-A2.
XX PD 05-DEC-2002.
XX PF 31-MAY-2002; 2002WO-DK000372.
XX PR 31-MAY-2001; 2001DK-00000859.
XX PR 05-JUL-2001; 2001US-0303180P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
XX DR WPI; 2003-041403/03.
XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
XX PT disorders.
XX PS Example 1; Fig 8; 52pp; English.
XX XX The invention relates to an isolated polypeptide comprising a 51 amino
XX CC acid sequence being a generic sequence for a Kunitz-type protease
XX CC inhibitor or a variant where the sequence is at least 80% identical to
XX CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
XX CC included are an isolated polypeptide obtainable by cultivation of a host
XX CC cell comprising a polynucleotide construct encoding kunitz-type protein
XX CC in an appropriate growth medium under conditions allowing expression of
XX CC the polynucleotide construct and recovering the polypeptide from the
XX CC culture medium, a polynucleotide construct encoding the kunitz-type
XX CC protein and a host cell comprising the polynucleotide construct. The
XX CC kunitz-type protein is used for the preparation of a medicament for the
XX CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
XX CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
XX CC haemorrhage, myocardial infarction, for prevention of blood loss during
XX CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, emphysema,
XX CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
XX CC inflammatory bowel disease, and psoriasis. The present sequence
XX CC represents a mutant human HKI-18 with a yeast 212L signal peptide and a
XX CC KEX-2 cleavage site, expressed in yeast cells

```

SQ	Sequence	111 AA;
OY	Query Match	95.4%; Score 314; DB 6; Length 111;
	Best Local Similarity	94.8%; Pred. No. 1.3e-29;
	Matches	55; Conservative 0; Mismatches 3; Indels 0; Gaps 0
DB	1 YPVCLLPPTGCKARIRFWFVAVGGCNPRVGGCGGNANPASDECMSSCGGS	58
	54 YPVCCLLPATGPCKAPAAWRFVAVGGCNPRVGGCGGNANPASDECMSSCGGS	111
RESULT 5		
ID	ABG71916	
XX	ABG71916 standard; protein; 58 AA.	
XX	ABG71916;	
DT	22-JAN-2003 (first entry)	
DE	Human Kunitz protease inhibitor protein HKI-18, mutant #3.	
XX	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;	
KW	anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;	
KM	systemic inflammatory response syndrome; acute pancreatitis;	
KW	shock syndrome; disseminated intravascular coagulation; mutant;	
KM	hyperfibrinolysis haemorrhage; myocardial infarction; mifein;	
KW	cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;	
KM	allergy-induced protease release; deep vein thrombosis;	
KX	adult respiratory distress syndrome; chronic inflammatory bowel disease.	
OS	Homo sapiens.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Misc-difference 9	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 11	/note= "Wild-type His substituted by Thr"
FT	Misc-difference 15..16	/note= "Wild-type Ala-Asp substituted by Lys-Ala"
PN	NC0200296938-A2.	
XX	05-DEC-2002.	
PD	31-MAY-2002; 2002MO-DK000372.	
PF	31-MAY-2001; 2001DK-00000859.	
PR	05-JUL-2001; 2001US-0303180P.	
XX	(NOVO) NOVO NORDISK AS.	
PA	Jorgensen MU, Bang S, Olsen OH, Petersen LC;	
PI	WPI; 2003-041403/03.	
DR		
XX		
PT	Kunitz-type protease inhibitor used in the treatment of inflammatory disorders.	
PS		
XX	Claim 20; Page 49; 52pp; English.	
CC	The invention relates to an isolated polypeptide comprising a 51 amino acid sequence being a generic sequence for a Kunitz-type protease inhibitor or a variant where the sequence is at least 80% identical to the kunitz domain of human kunitz type protease inhibitor HKI-18. Also included are an isolated polypeptide construct encoding cultivation of a host cell comprising a polynucleotide construct encoding kunitz-type protein in an appropriate growth medium under conditions allowing expression of the polynucleotide construct and recovering the polypeptide from the culture medium, a polynucleotide construct encoding the kunitz-type protein and a host cell comprising the polynucleotide construct. The kunitz-type protein is used for the preparation of a medicament for the treatment of systemic inflammatory response syndrome, acute pancreatitis,	

CC	shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
CC	haemorrhage, myocardial infarction, for prevention of blood loss during
CC	major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
CC	allergy-induced protease release, deep vein thrombosis, emphysema,
CC	rheumatoid arthritis, adult respiratory distress syndrome, chronic
CC	inflammatory bowel disease, and psoriasis. The present sequence is a
CC	human HKI-18 mutant sequence
XX	
SQ	Sequence 58 AA;
Db	
Qy	1 YPVACLLPPTATGCKARIIRWYFVASVGGCGRNFYVGCGRGANNFASOECSMSSCOGS 58 1 YPVACLLPPTATGSKAMAAARWFVASVGGCRNRFYVGCGHGMANNFASOECSMSSCOGS 58
RESULT 6	
ID	ABG71919 standard; protein; 111 AA.
XX	
AC	ABG71919;
XX	
DT	22-JAN-2003 (first entry)
XX	
DE	Human 212L-HKI-18-1 fusion protein.
XX	
KM	Human, protease inhibitor, kunitz; HKI-18; antiinflammatory; mutant;
KM	anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema; mutein;
KM	systemic inflammatory response syndrome; acute pancreatitis;
KM	shock syndrome; disseminated intravascular coagulation; yeast;
KM	hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
KM	cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
KM	allergy-induced protease release; deep vein thrombosis;
KM	adult respiratory distress syndrome; chronic inflammatory bowel disease.
XX	
OS	Homo sapiens.
OS	Saccharomycetes cerevisiae.
OS	Synthetic.
OS	Chimeric.
XX	
FT	Key Location/Qualifiers
FT	Peptide 1..51
FT	/label= 212L_signal_peptide
FT	Cleavage-site 52..53
FT	/label= KEX2_cleavage_site
FT	Protein 54..111
FT	/label= HKI_18
FT	Misc-difference 62
FT	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 64
FT	/note= "Wild-type His substituted by Thr"
FT	Misc-difference 68..69
FT	/note= "Wild-type Ala-Asp substituted by Lys-Ala"
PX	
PN	MO200296938-A2.
XX	
XX	
PD	05-DEC-2002.
XX	
PF	31-MAY-2002; 2002MO-DK000372.
XX	
PR	31-MAY-2001; 2001DK-000000859.
PR	05-JUL-2001; 2001US-0303180P.
XX	
XX	(NOVO) NOVO NORDISK AS.
PI	Jorgensen MU, Bang S, Olsen OH, Petersen LC;
XX	
DR	WPI; 2003-041403/03.
XT	Kunitz-type protease inhibitor used in the treatment of inflammatory

PT disorders.
 XX
 PS Example 1; Fig 8; 52pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 51 amino
 CC acid sequence being a generic sequence for a Kunitz-type protease
 CC inhibitor or a variant where the sequence is at least 80% identical to
 CC the Kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 CC included are an isolated polypeptide obtainable by cultivation of a host
 CC cell comprising a polynucleotide construct encoding kunitz-type protein
 CC in an appropriate growth medium under conditions allowing expression of
 CC the polynucleotide construct and recovering the polypeptide from the
 CC culture medium, a polynucleotide construct encoding the kunitz-type
 CC protein and a host cell comprising the polynucleotide construct. The
 CC kunitz-type protein is used for the preparation of a medicament for the
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 CC hemorrhage, myocardial infarction, for prevention of blood loss during
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, emphysema,
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
 CC inflammatory bowel disease, and psoriasis. The present sequence
 CC represents a mutant human HKI-18 with a yeast 212L signal peptide and a
 CC KEX-2 cleavage site, expressed in yeast cells
 XX
 SQ Sequence 111 AA;
 Query Match 88.4%; Score 291; DB 6; Length 111;
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGCGRCGNANNFASBQECMSSCGSS 58
 Db 54 YPVRCILPPATGSKAMAAWRYFVASVGQCNRFVYGCGRCGNANNFASBQECMSSCGSS 111
 XX
 RESULT 7
 AAB60623
 ID AAB60623 standard; protein; 58 AA.
 XX
 AC AAB60623;
 XX
 DT 27-APR-2001 (first entry)
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID NO:1.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
 KW proteinase-3 inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW platelet activation; blood coagulation; neutrophil activation;
 KW monocyte activation; angioplasty; inflammatory disease; lung injury;
 KW vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PR 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/) DAVIES C.
 PA (CHEN/) CHEN D.
 PA (ROCZ/) ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznik S;
 XX
 DR WPI; 2001-190860/19.
 DR N-PSDB; AAF59750.
 XX

PT Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
 PT for treating emphysema, cystic fibrosis, adult respiratory distress
 PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX
 PS Claim 6; Col 9-10; 17pp; English.
 XX
 CC The invention relates to a novel human serine protease inhibitor of the
 CC Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
 CC AAB60634). The BTL.010 protein is thought to preferentially inhibit
 CC neutral serine proteases such as elastase and proteinase-3, relative to
 CC trypsin-like and chymotrypsin-like proteases. A substantial proportion of
 CC the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
 CC searching in the Genbank high throughput genomic (HTG) DNA sequence
 CC database using the Kunitz domain sequences AAB60630, and was confirmed as
 CC being novel using the Kunitz domain sequences AAB60632, and AAB60633.
 CC This sequence information was extended to provide a larger region of
 CC BTL.010 protein sequence data (AAB60634) by identifying an open reading
 CC frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
 CC fragment in a 399 bp fragment of human genomic DNA (AAF59750).
 CC corresponding to bases 16016-16414 of Genbank accession number AC004846.
 CC The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
 CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
 CC compositions comprising it, may be used for inhibiting protease activity,
 CC particularly that of leukocyte elastase, in the prevention, treatment or
 CC amelioration of medical conditions such as emphysema, idiopathic
 CC pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
 CC rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
 CC compositions of the invention modulate at least one physiological
 CC condition such as platelet activation, blood coagulation, neutrophil
 CC activation, or monocyte activation. BTL.010 is also useful for the
 CC prophylactic or therapeutic treatment of patients undergoing angioplasty,
 CC and for the treatment of inflammatory diseases and diseases involving
 CC lung and vascular injury. The present sequence represents the human
 CC BTL.010 protease inhibitor Kunitz domain
 XX
 SQ Sequence 58 AA;
 Query Match 80.2%; Score 264; DB 4; Length 58;
 Best Local Similarity 82.8%; Pred. No. 6.3e-24;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGCGRCGNANNFASBQECMSSCGSS 58
 Db 1 YPVRCILPSAHGSCADWAAWRYFVASVGQCNRFVYGCGRCGNANNFASBQECMSSCGSS 58
 XX
 RESULT 8
 ABG71912
 ID ABG71912 standard; protein; 58 AA.
 XX
 AC ABG71912;
 XX
 DT 22-JAN-2003 (first entry)
 DE Human Kunitz protease inhibitor protein HKI-18.
 XX
 KW Human; protease inhibitor; kunitz; HKI-18; anti-inflammatory;
 KW anticoagulant; coagulant; cardiac; CPB; psoriasis; emphysema;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation;
 KW hyperfibrinolytic haemorrhage; myocardial infarction;
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
 KW allergy-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5..55
 FT /label= Kunitz_domain
 FT /note= "This domain is claimed in claim 18"
 XX
 PN WO200296938-A2.

```

XX 05-DEC-2002.
PD
XX
XX 31-MAY-2002; 2002MO-DK000372.
PF
XX 31-MAY-2001; 2001DK-00000859.
PR
XX 05-JUL-2001; 2001US-0303180P.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Jorgensen MU, Bang S, Olsen OH, Petersen LC;
PI
XX MPI: 2003-041403/03.
XX
XX N-PSDB; ABS56455.
XX
XX Kunitz-type protease inhibitor used in the treatment of inflammatory
PT disorders.
XX
XX Claim 19; Fig 2; 52pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a 51 amino
CC acid sequence being a generic sequence for a Kunitz-type protease
CC inhibitor or a variant where the sequence is at least 80% identical to
CC the Kunitz domain of human Kunitz type protease inhibitor HKI-18. Also
CC included are an isolated polypeptide obtainable by cultivation of a host
CC cell comprising a polynucleotide construct encoding Kunitz-type protein
CC in an appropriate growth medium under conditions allowing expression of
CC the polynucleotide construct and recovering the polypeptide from the
CC culture medium, a polynucleotide construct encoding the Kunitz-type
CC protein and a host cell comprising the polynucleotide construct. The
CC Kunitz-type protein is used for the preparation of a medicament for the
CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
CC haemorrhage, myocardial infarction, for prevention of blood loss during
CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, emphysema,
CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
CC inflammatory bowel disease, and psoriasis. The present sequence is human
CC HKI-18
XX
XX
SQ Sequence 58 AA;

Query Match      80.2%; Score 264; DB 6; Length 58;
Best Local Similarity 82.8%; Pred. No. 6.3e-24;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSCGGS 58
    |||||
DB 1 YPVRCILPPAHSGCADMARMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSCGGS 58

RESULT 9
ADL16831
ID ADL16831 standard; peptide; 58 AA.
XX
XX ADL16831;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Human BTL.010 protein Kunitz domain (KD) peptide.
DE
XX
XX BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KW inflammatory disease; oxidative burst; platelet activation;
KW blood coagulation; gene therapy; human; KD.
XX
XX Homo sapiens.
OS
XX US6689582-B1.
PN
XX 10-FEB-2004.
XX

```

```

PF 12-MAY-2000; 2000US-00569670.
XX
XX 05-AUG-1999; 99US-00369494.
XX
XX (FARB ) BAYER PHARM CORP.
XX
XX Davies C, Chen D, Rocznik S;
PI
XX MPI: 2004-141424/14.
XX
XX New isolated polynucleotide encoding BTL.010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
PT glomerulonephritis.
XX
XX Claim 1; SEQ ID NO 1; 17pp; English.
XX
XX The invention relates to BTL.010, a human serine proteinase inhibitor of
CC the Kunitz family and its corresponding nucleic acid sequence. The
CC sequences of the invention are useful for treating diseases, e.g.
CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
CC sequence is human BTL.010 protein Kunitz domain (KD) peptide.
XX
XX
SQ Sequence 58 AA;

Query Match      80.2%; Score 264; DB 8; Length 58;
Best Local Similarity 82.8%; Pred. No. 6.3e-24;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSCGGS 58
    |||||
DB 1 YPVRCILPSAHSGCADMARMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSCGGS 58

RESULT 10
ABG71918
ID ABG71918 standard; protein; 111 AA.
XX
XX ABG71918;
AC
XX 22-JAN-2003 (first entry)
DT
XX
XX Human HKI-18/212L signal peptide.
DE
XX
XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
KW anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;
KW systemic inflammatory response syndrome; acute pancreatitis;
KW shock syndrome; disseminated intravascular coagulation; yeast;
KW hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
KW allergy-induced protease release; deep vein thrombosis;
KW adult respiratory distress syndrome; chronic inflammatory bowel disease.
XX
XX Homo sapiens.
OS
XX Saccharomyces cerevisiae.
OS
XX Synthetic.
OS
XX Chimeric.
XX
XX Key Location/Qualifiers
FH Peptide 1..51
FT /label= 212L_signal_peptide
FT Cleavage-site 52..53
FT /label= KEX2_cleavage_site
FT Protein 54..111
FT /label= HKI_18
XX
XX WO200296938-A2.
XX

```


KM idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KM cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KM inflammatory disease; oxidative burst; platelet activation;
 KM blood coagulation; gene therapy.
 XX
 XX
 OS Unidentified.
 PH
 FT
 PT
 PT
 XX
 XX
 PN US6689582-B1.
 XX
 XX 10-FEB-2004.
 PD
 PF 12-MAY-2000; 2000US-00569670.
 XX
 XX
 PR 05-AUG-1999; 99US-00369494.
 XX
 PA (FARB) BAYER PHARM CORP.
 XX
 PI Davies C, Chen D, Rocznik S;
 XX
 XX WPI; 2004-141424/14.
 DR
 XX
 XX
 PT New isolated polynucleotide encoding BTL010 serine proteinase, useful
 PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
 PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
 PT glomerulonephritis.
 XX
 PS Disclosure; SEQ ID NO 15; 17bp; English.
 CC
 CC The invention relates to BTL010, a human serine proteinase inhibitor of
 CC the Kunitz family and its corresponding nucleic acid sequence. The
 CC sequences of the invention are useful for treating diseases, e.g.
 CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
 CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
 CC glomerulonephritis or inflammatory diseases. The BTL010 protein is also
 CC useful for preventing neutrophil and monocyte activation and formation of
 CC active oxygen species during the oxidative burst of stimulated
 CC granulocytes. It is also useful for reducing platelet activation and
 CC blood coagulation. BTL010 DNA is useful in gene therapy. The present
 CC sequence is a BTL010 protein related protein.
 CC
 XX
 SQ Sequence 189 AA;
 QY
 DB 1 YPVRCILPPATGPKARIRIWFVAVSGQCNRFVYGGCGNANNPASBECMSSCGGS 58
 10 YPVRCILPPAHSGSCADMAARWVFVAVSGQCNRFWYGGCHGNANNPASBECMSSCGGS 67
 RESULT 13
 ID ADO55146 standard; protein; 1235 AA.
 XX
 AC ADO55146;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX
 XX Protein #48 with increased gene expression in renal cell carcinoma.
 DE
 XX
 XX
 KM cytotatic; gene therapy; differential expression; renal cell carcinoma;
 KM clear cell RCC; papillary RCC; chromophobe/oncocytoma RCC;
 KM sarcomatoid RCC; TCC; Wilms' tumor; gene expression; kidney cancer;
 KM diagnostic marker; cancer.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO2004032842-A2.

XX
 PD 22-APR-2004.
 XX
 PF 06-OCT-2003; 2003WO-US031476.
 XX
 XX
 PR 04-OCT-2002; 2002US-0415775P.
 XX
 PA (VAND-) VAN ANDEL INST.
 XX
 PI Teh BT, Takahashi M;
 XX
 XX WPI; 2004-340789/31.
 DR
 XX N-PSDB; ADO54960.
 XX
 XX New nucleic acid and polypeptide compositions, useful in the field of
 PT molecular biology and medicine, in particular for gene expression
 PT profiling, identifying diagnostic markers, and treating certain types of
 PT kidney cancer.
 XX
 PS Example IV; SEQ ID NO 243; 53bp; English.
 XX
 CC The invention relates to novel genes that are differentially expressed in
 CC sub-types of renal cell carcinomas and methods of detecting them using
 CC nucleic acids and probes. The nucleic acid probes hybridize with part or
 CC all of a coding sequence that is overexpressed in clear cell renal cell
 CC carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC,
 CC sarcomatoid RCC, TCC, or Wilms' tumors, which overexpression is based on
 CC comparison to a baseline value. The methods and compositions of the
 CC present invention are useful in the field of molecular biology and
 CC medicine, in particular for gene expression profiling of certain types of
 CC kidney cancer, in identifying diagnostic markers, and treating such
 CC cancer patients. This sequence corresponds to the protein encoded by a
 CC gene with increased expression in CC-RCC.
 CC
 XX
 SQ Sequence 1235 AA;
 QY
 DB 1 YPVRCILPPATGPKARIRIWFVAVSGQCNRFVYGGCGNANNPASBECMSSCGGS 58
 688 YPVRCILPPAHSGSCADMAARWVFVAVSGQCNRFWYGGCHGNANNPASBECMSSCGGS 745
 RESULT 14
 ID ABR58408 standard; protein; 1280 AA.
 XX
 AC ABR58408;
 XX
 XX 07-JUL-2003 (first entry)
 DT
 XX
 XX Human NOV22a.
 DE
 XX
 XX Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
 KM immunomodulator; cytotatic; neurotropic; neuroprotective; dyslipidaemia;
 KM antiparkinsonian; antidiabetic; gene therapy; metabolic disorder;
 KM diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
 KM neurodegenerative disorder; Alzheimer's disease; immune disorder;
 KM haematopoietic disorder.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO2003029423-A2.
 XX
 XX 10-APR-2003.
 PD
 PF 02-OCT-2002; 2002WO-US031358.
 XX
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327342P.
 PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 12-APR-2002; 2002US-031972P.
PR 12-APR-2002; 2002US-031980P.
PR 17-APR-2002; 2002US-033281P.
PR 19-APR-2002; 2002US-0373805P.
PR 23-APR-2002; 2002US-0374738P.
PR 16-MAY-2002; 2002US-0381101P.
PR 17-MAY-2002; 2002US-0381635P.
PR 29-MAY-2002; 2002US-0383830P.
PR 01-OCT-2002; 2002US-00262839.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E;
PI Binger SR, Elleman K, Gerlach VL, Gorman L, Guo X, Ji W, Ju D;
PI Kerkula R, Leach MD, Li L, Miller CE, Paturajan M, Rieger RK;
PI Rothenberg ME, Shimkets RA, Smithson G, Spytek KA, Taupier RJ;
PI Vernet CM, Voss EZ, Zernhagen BD, Zhong M;

DR WPI; 2003-381625/36.
DR N-PSDB; ACC72120.

PT NOVX polypeptides and nucleic acids useful for diagnosing, preventing or
PT treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or
PT dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

PS Claim 1; Page 177; 487Pp; English.

XX The present invention relates to novel human NOV proteins and their
XX coding sequences (ACCT2075-ACC72181 and ABR58363-ABR58469). The NOV
XX proteins are useful in manufacturing a medicament for treating a syndrome
XX associated with a human disease. The NOV proteins and coding sequences
XX may be used to diagnose, treat or prevent metabolic disorders such as
XX diabetes or obesity, infections, cachexia, cancer, neurodegenerative
XX disorders such as Alzheimer's disease or Parkinson's disease, immune
XX disorders, haematopoietic disorders and various dyslipidaemias

SQ Sequence 1280 AA;

Query Match 80.2%; Score 264; DB 6; Length 1280;
Best Local Similarity 82.8%; Pred. No. 1,4e-22;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 YPVRCLLPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNPASBQECSSCGS 58
DB 752 YPVRCLLPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNPASBQECSSCGS 809

RESULT 15
AAB60631

ID AAB60631 standard; protein; 51 AA.

XX AAB60631;

XX (27-APR-2003) (first entry)

DE Human BTL-010 Kunitz domain fragment, SEQ ID NO:9.

KW Human BTL-010; neutral serine protease inhibitor; elastase inhibitor;
KW proteinase-3 inhibitor; Kunitz domain; emphysema;
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

KW platelet activation; blood coagulation; neutrophil activation;
KW monocyte activation; angioplasty; inflammatory disease; lung injury;
KW vascular injury; nephrotropic; antirheumatic; antiarthritic.

OS Homo sapiens.

PN US6180607-B1.

PD 30-JUN-2001

PF 05-AUG-1999; 99US-00369494.

PR 05-AUG-1999; 99US-00369494.

PA (DAVI/) DAVIES C.

PA (CHEN/) CHEN D.

PI Davies C, Chen D, Rocznik S;

DR WPI; 2001-190860/19.

DR N-PSDB; AAF59750.

PT Novel serine proteinase inhibitor of the Kunitz family, BTL-010 useful
PT for treating emphysema, cystic fibrosis, adult respiratory distress
PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
PS Disclosure; Col 5-6; 17pp; English.

XX The invention relates to a novel human serine protease inhibitor of the
XX Kunitz family, BTL-010 (fragments given in AAB60623, AAB60631 and
XX AAB60634). The BTL-010 protein is thought to preferentially inhibit
XX neutral serine proteases such as elastase and proteinase-3, relative to
XX trypsin-like and chymotrypsin-like proteases. A substantial proportion of
XX the BTL-010 protein Kunitz domain (AAB60631) was identified via homology
XX searching in the Genbank high throughput genomic (HTG) DNA sequence
XX database using the Kunitz domain sequences AAB60630, and AAB60633.
XX This sequence information was extended to provide a larger region of
XX BTL-010 protein sequence data (AAB60634) by identifying an open reading
XX frame (ORF) which comprised DNA encoding the BTL-010 Kunitz domain
XX fragment in a 399 bp fragment of human genomic DNA (AAF59750), AC004846.
XX Corresponding to bases 16016-16414 of Genbank accession number AAB60623.
XX The entire BTL-010 Kunitz domain sequence (AAB60623) was obtained from
XX the BTL-010 ORF-encoded sequence. The BTL-010 protein, and pharmaceutical
XX compositions comprising it, may be used for inhibiting protease activity,
XX particularly that of leukocyte elastase, in the prevention, treatment or
XX amelioration of medical conditions such as emphysema, idiopathic
XX pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
XX rheumatoid arthritis, organ failure or glomerulonephritis. BTL-010
XX compositions of the invention modulate at least one physiological
XX condition such as platelet activation, blood coagulation, neutrophil
XX activation, or monocyte activation. BTL-010 is also useful for the
XX prophylactic or therapeutic treatment of patients undergoing angioplasty,
XX and for the treatment of inflammatory diseases and diseases involving
XX lung and vascular injury. The present sequence represents a substantial
XX proportion of the human BTL-010 protease inhibitor Kunitz domain

SQ Sequence 51 AA;

Query Match 67.0%; Score 220.5; DB 4; Length 51;
Best Local Similarity 80.8%; Pred. No. 8.7e-19;
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

OY 5 CLIPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNPASBQECSSCGS 56
DB 1 CLIPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNPASBQECSSCGS 51

Search completed: August 25, 2005, 04:52:21
Job time : 168 secs

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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:48:01 ; Search time 16 Seconds
(without alignments)
348.786 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329

Sequence: 1 YPVRCILPPATGPKARIIR.....RGNNPFASQECMSQGS 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	192	58.4	100 1	TIBO basic proteinase i
2	190	57.8	59 2	S00371 isoaprotinin G1 -
3	188	57.1	58 2	S10063 isoaprotinin G2 -
4	184	55.9	60 1	TIBOR serum basic protei
5	184	55.9	100 1	TIBOSP spleen basic prote
6	174	52.9	122 1	A55115 uterine plasmin/tr
7	168	51.1	111 2	S41082 amyloid precursor
8	168	51.1	751 2	A49974 beta-amyloid precu
9	168	51.1	763 2	A49321 amyloid beta (A4)
10	168	51.1	765 2	S42880 amyloid precursor-
11	164	49.8	61 1	TIIVIT1 venom basic protei
12	163	49.5	57 2	A59204 basic proteinase i
13	163	49.5	62 2	A44180 taicetoxin serine
14	163	49.5	110 1	TIITOR basic proteinase i
15	161	48.9	249 2	T32060 hypohetrical prote
16	159	48.3	61 2	TIHCBP proteinase inhibit
17	159	48.3	62 2	S07451 proteinase inhibit
18	159	48.3	252 2	JG0185 hepatocyte growth
19	158	48.0	58 1	TIHAKK isochinhibitor K (BP
20	158	48.0	76 2	S06678 Alzheimer's diseas
21	158	48.0	76 2	S03607 Alzheimer's diseas
22	158	48.0	484 4	A32761 hypohetrical Alzhe
23	158	48.0	770 1	QRHDA4 Alzheimer's diseas
24	157	47.7	76 2	S04855 Alzheimer's diseas
25	157	47.7	100 2	A32282 Alzheimer's diseas
26	156	47.4	2235 2	T26063 hypohetrical prote
27	155	47.1	747 2	JH0773 Alzheimer's diseas
28	154	46.8	123 2	A29652 inter-alpha-trypsi
29	152	46.2	265 2	A53390 Kunitz-type protei

30	152	46.2	349 2	S21089 alpha-1-microglobu
31	151	45.9	62 2	S19327 venom basic protei
32	151	45.9	125 1	TIHOB1 alpha-1-microglobu
33	151	45.9	349 2	S35708 alpha-1-microglobu
34	151	45.9	352 1	TIHOB1 alpha-1-microglobu
35	150	45.6	67 1	TIBOC trypsin inhibitor,
36	148	45.0	64 2	S41399 Kunitz-type protei
37	148	45.0	65 1	TIIVVC venom basic protei
38	148	45.0	38 2	A54951 tissue factor path
39	148	45.0	235 2	C89114 protein C37C3.6a f
40	148	45.0	2167 2	T34395 hypohetrical prote
41	147	44.7	304 1	TIHUGK tissue factor path
42	145	44.1	352 1	HCHU alpha-1-microglobu
43	145	44.1	922 2	T23573 hypohetrical prote
44	144	43.8	57 1	TIHVC venom basic protei
45	144	43.8	302 1	TIHUGK tissue factor path

ALIGNMENTS

RESULT 1
TIBO
basic proteinase inhibitor precursor - bovine
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPT; cationic kallikrein; Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence revision 22-Jul-1994 #ext change 09-Jul-2004
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A20203; A90927; A346
R:Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987
A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibi
A:Reference number: S00274; PMID:87283904; PMID:2441071
A:Accession: S00277
A:Molecule type: DNA; mRNA
A:Residues: 1100 <CR2>
A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; I
R:Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
A:Reference number: A90926; PMID:88295740; PMID:2456884
A:Accession: A30333
A:Molecule type: DNA
A:Residues: 1-100 <CRE>
A:Cross-references: GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; PID:G162769
R:Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic er
A:Reference number: S10546; PMID:86158754; PMID:2420326
A:Accession: S10546
A:Molecule type: DNA
A:Residues: 34-97 <KIN>
R:Piorretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
A:Title: Aprotinin-like isochinhibitors in bovine organs.
A:Reference number: S02485; PMID:89076531; PMID:2462435
A:Accession: S02486
A:Molecule type: protein
A:Residues: 36-93 <RIO>
R:Ilekita, M.; Jone, C.S.; Kamo, M.; Tsugita, A.; Kiukki, K.; Moriya, H.
Protein Seq. Data Anal. 5, 7-11, 1992
A:Title: Purification and characterization of the major cationic kallikrein inhibitor in
A:Reference number: S28197; PMID:93150003; PMID:1283464
A:Accession: S28197
A:Molecule type: protein
A:Residues: 36-93 <IKK>
R:Kasaeli, B.; Laskowski, M.
Biochem. Biophys. Res. Commun. 20, 463-468, 1965
A:Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
A:Reference number: A90162; PMID:66083012; PMID:5860161
A:Contents: annotation; disulfide bonds
A:Accession: A90162
A:Molecule type: protein
A:Residues: 36-93 <KAS>

R.Anderer, F.A.; Hornle, S.
 J. Biol. Chem. 241, 1568-1572, 1966
 A>Title: The disulfide linkages in kallikrein inactivator of bovine lung.
 A:Reference number: A92023; PMID:6171231; PMID:5296424
 A:Contents: annotation; disulfide bonds
 A:Accession: A92023
 A:Molecule type: protein
 A:Residues: 36-93 <AN2>
 R:Chavet, J.; Acher, R.
 Bull. Soc. Chim. Biol. 49, 985-1000, 1967
 A>Title: La structure covalente d'un inhibiteur polypeptidique de la trypsine (inhibiteur
 A:Reference number: A90736; PMID:68012003; PMID:6053204
 A:Contents: annotation; disulfide bonds
 A:Accession: A90736
 A:Molecule type: protein
 A:Residues: 36-93 <CHA>
 R:Jolova, V.; Pospisilova, D.; Meloun, B.; Som, F.
 Collect. Czech. Chem. Commun. 33, 1363-1365, 1968
 A>Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
 A:Reference number: A90927
 A:Accession: A90927
 A:Molecule type: protein
 A:Residues: 36-93 <DLO>
 R:Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H.
 Naturwissenschaften 57, 389-392, 1970
 A>Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and confi
 A:Reference number: A93410; PMID:70255230; PMID:5447861
 A:Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstroms
 R:Lewis, R.V.; Ray, P.; Coghill, R.; Kruggel, W.
 Biochem. Biophys. Res. Commun. 167, 543-547, 1990
 A>Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells.
 A:Reference number: A34658; PMID:90211226; PMID:2322242
 A:Accession: A34658
 A:Molecule type: protein
 A:Residues: 36-53, 55-81 <LEM>
 R:Anderson, S.; Kingston, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983
 A>Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a
 A:Reference number: A93977; PMID:84070725; PMID:6580617
 A:Accession: A93977
 A:Molecule type: DNA
 A:Residues: 'PSLENRDPPIPA', 34-97, 'GKTGGRABEGRGK' <AND>
 A:Cross-references: GB:X03365; GB:X00966; NID:9142; PID:CAA27062.1; PID:G1364183
 R:Stekmann, J.; Wenzel, H.R.; Schroeder, W.; Teschsch, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A>Title: Characterization and sequence determination of six aproctinin homologues from bo
 A:Reference number: S00371; PMID:88221840; PMID:2453200
 A:Accession: S10063
 A:Molecule type: protein
 A:Residues: 36-66, 'P', 68-82, 'S', 84-93 <SIE>
 A:Experimental source: lung
 A:Note: the authors designated this protein as isoaprotinin 2
 C:Comment: Basic proteinase inhibitor is an intracellular polypeptide found in many tiss
 C:Genetics:
 A:introns: 34/1, 98/1
 C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor
 F:1-20/Domains: signal sequence #status predicted <SIG>
 F:21-35/Domains: propeptide #status predicted <PRO>
 F:36-100/Product: basic proteinase inhibitor #status experimental <MAT>
 F:40-80/Domains: animal kunitz-type proteinase inhibitor homology <BPI>
 F:50/Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experimen

Query Match 58.4%; Score 192; DB 1; Length 100;
 Best Local Similarity 57.9%; Pred. No. 2.5e-16;
 Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 PYRCLLPATGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 58
 DB 37 PDCLEPPYTGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 59

RESULT 2
 S00371
 isoaprotinin G1 - bovine hybrid
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C:Accession: S00371
 R:Stekmann, J.; Wenzel, H.R.; Schroeder, W.; Teschsch, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A>Title: Characterization and sequence determination of six aproctinin homologues from bo
 A:Reference number: S00371; PMID:88221840; PMID:2453200
 A:Accession: S00371
 A:Molecule type: protein
 A:Residues: 1-59 <SIE>
 A:Cross-references: UNIPROT:Q7M311
 C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
 C:Keywords: pyroglutamic acid; serine proteinase inhibitor
 F:6-56/Domains: animal kunitz-type proteinase inhibitor homology <BPI>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 57.8%; Score 190; DB 2; Length 59;
 Best Local Similarity 56.1%; Pred. No. 2.7e-16;
 Matches 32; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 PYRCLLPATGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 58
 DB 3 PDCLEPPYTGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 59

RESULT 3
 S10063
 isoaprotinin G2 - bovine hybrid
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C:Accession: S10063
 R:Stekmann, J.; Wenzel, H.R.; Schroeder, W.; Teschsch, H.
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
 A>Title: Characterization and sequence determination of six aproctinin homologues from bo
 A:Reference number: S00371; PMID:88221840; PMID:2453200
 A:Accession: S10063
 A:Molecule type: protein
 A:Residues: 1-58 <SIE>
 A:Cross-references: UNIPROT:Q7M312
 C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor
 F:5-55/Domains: animal kunitz-type proteinase inhibitor homology <BPI>
 F:15/Inhibitory site: Lys (trypsin) #status predicted

Query Match 57.1%; Score 188; DB 2; Length 58;
 Best Local Similarity 56.1%; Pred. No. 4.7e-16;
 Matches 32; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 PYRCLLPATGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 58
 DB 2 PDCLEPPYTGPKAKIRIRWYFVASVGQCNRFYVGGCGGNANFPASBEOCMSSCGGS 59

RESULT 4
 TIBOR
 serum basic proteinase inhibitor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
 C:Accession: A01206
 R:Wachter, E.; Depner, K.; Hochstrasser, K.; Lempart, K.; Gelger, R.
 FEBS Lett. 119, 58-62, 1980
 A>Title: A new kunitz-type inhibitor from bovine serum amino acid sequence determination.
 A:Reference number: A01206; PMID:8104408; PMID:7428928
 A:Accession: A01206
 A:Molecule type: protein
 A:Residues: 1-60 <MAC>
 A:Cross-references: UNIPROT:P00975
 C:Comment: This inhibitor has activity very similar to that of the basic protease inhibi
 C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol


```

A/Molecule type: DNA
A/Residues: 1-111 <PRT>
A/Cross-references: UNIPROT:Q7M4L3
F:59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 51.1%; Score 168; DB 2; Length 111;
Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKKARIIRWYFVASVGQCNRFYGGCGGNANPFASBOECMSSCQ 56
Db 59 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNPFESBDCMAVCK 110

RESULT 8
beta-amyloid precursor protein 2 homolog APRP2 - mouse
A/Accession: A49974
C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49974
R/Status: H.H.; Talmakara, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A/Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A/Reference number: A49974; MUID:94132029; PMID:8300594
A/Accession: A49974
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-751 <SLU>
A/Cross-references: UNIPROT:Q60709; GB:U1571; NID:9558467; PIDN:AA50603.1; PID:g558468
A/Note: sequence extracted from NCBI backbone (NCBI:P:144636)
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
F:110-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 51.1%; Score 168; DB 2; Length 751;
Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKKARIIRWYFVASVGQCNRFYGGCGGNANPFASBOECMSSCQ 56
Db 310 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNPFESBDCMAVCK 361

RESULT 9
amyloid beta (A4) homolog 2 precursor - human
A/Accession: A49321
N/Alternate names: CDE1-binding protein
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49321; S34644; S40519
R/Sprecher, C.A.; Grant, F.U.; Grimm, G.; O'Hara, P.U.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A/Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A/Reference number: A49321; MUID:93250009; PMID:8485127
A/Accession: A49321
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <SPR>
A/Cross-references: UNIPROT:Q06481; GB:S60099; NID:9300168; PIDN:AA60589.1; PID:g300169
A/Experimental source: placenta
A/Note: sequence extracted from NCBI backbone (NCBI:N:131198, NCBI:P:131199)
A/Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R/von der Kammer, H.; Kladinsky, J.; Hanes, J.; Scheitel, K.H.
submitted to the EMBL Data Library, April 1993
A/Description: The human homologue of the murine CDE1 binding protein is an amyloid prec
A/Reference number: S34644
A/Accession: S34644
A/Molecule type: mRNA
A/Residues: 1-763 <YON>
A/Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R:Nasos, W.; Gurtubagavatu, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A/Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A/Reference number: S40519; MUID:94053131; PMID:8220435

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A/Accession: S40519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <WAS>
A/Cross-references: GB:L27631; NID:g450391; PIDN:AA61701.1; PID:g450392
C/Genetic:
A/Genes: GDB:APLP2; APLP2
A/Cross-references: GDB:139159; OMIM:104776
A/Map position: 11q23-11q25
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C/Keywords: alternative splicing; transmembrane protein
F:110-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 51.1%; Score 168; DB 2; Length 763;
Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKKARIIRWYFVASVGQCNRFYGGCGGNANPFASBOECMSSCQ 56
Db 310 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNPFESBDCMAVCK 361

RESULT 10
amyloid precursor-like protein - rat
A/Accession: S42880
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42880; S47528
R/Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A/Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precurs
A/Reference number: S42880
A/Accession: S42880
A/Molecule type: mRNA
A/Residues: 1-765 <SAN>
A/Cross-references: UNIPROT:P15943; EMBL:X77934
R/Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A/Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein prec
A/Reference number: S47528; MUID:94368849; PMID:8086458
A/Accession: S47528
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-765 <SA2>
A/Cross-references: EMBL:X77934
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C/Keywords: alternative splicing
F:112-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 51.1%; Score 168; DB 2; Length 765;
Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKKARIIRWYFVASVGQCNRFYGGCGGNANPFASBOECMSSCQ 56
Db 312 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNPFESBDCMAVCK 363

RESULT 11
venom basic proteinase inhibitor I - western sand viper
N/Alternate names: venom trypsin inhibitor I
C/Species: Vipera ammodytes ammodytes (western sand viper)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C/Accession: A01222
R/Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 740, 429-435, 1983
A/Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.
A/Reference number: A01222; MUID:84053385; PMID:6639951
A/Accession: A01222
A/Molecule type: protein
A/Residues: 1-61 <RT>
A/Cross-references: UNIPROT:P00991

```

C.Comment: This protein inhibits trypsin and kallikrein.
C.Superfamily: basic proteinase inhibitor; animal knittz-type proteinase inhibitor homo
C.Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
P.7-57/Domains: animal knittz-type proteinase inhibitor homology <BPI>
P.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
P.7-57,16-40,32-55/Disulfide bonds: #status predicted
P.11/Inhibitory site: lys (trypsin) #status predicted

Query Match	49.8%	Score 164	DB 1	Length 61
Best Local Similarity	48.3%	Pred. No. 4.2e-13		
Matches 28	Conservative 10	Mismatches 20	Indels 0	Gaps 0

[illegible]

RESULT 12

basic proteinase inhibitor - great pond snail
N:Alternate names: trypsin inhibitor
C:Species: *Lymanaea stagnalis* (great pond snail)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C:Accession: A59204
R:Nagle, G.
submitted to the Protein Sequence Database, March 2000
A:Description: *Lymanaea trypsin* inhibitor.
A:Reference number: A59204

A:Molecule type: protein
A:Residues: 1-57 <NAG>
A:Cross-references: UNIPROT:Q7M4I1
A:Experimental source: albumen gland
C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homo
C:Keywords: glycoprotein; serine proteinase inhibitor
F:5-55/Domain: animal kunitz-type proteinase inhibitor homology <BPT>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted
F:15/Inhibitory site: Lys (tryptan) #status predicted
F:24/Binding site: carbonylcarate (Asn) (covalent) #status experimental

Qy 5 CLLPATGPKKARIIRWYFVASVGQCNRFFVYGGCRGNANNFASEQECMS SC 55
| | | | | : : : : | : | | | | : : : :
Db 5 CSLPBTGPKCKGNFLRHYHNSSTNACDSFVYGGCKGNANNFQDIDDC KAC 55

RESULT 13

A44180
taicetoxin serine proteinase inhibitor component - Australian taipan
C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44180
R:Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Garroloa, G.
Toxicon 30, 1343-1364, 1992
A:Title: Isolation and physiological characterization of taicetoxin, a complex toxin with
A:Reference number: A44180; MUID:93134601; PMID:1485334
A:Accession: A44180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Cross-references: UNIPROT:Q7LZE4
A:Experimental source: subsp. scutellatus, venom (NCBI:122482)
A:Note: sequence extracted from NCBI backbone
C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
C:7-57/domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match	49.5%	Score 163	DB 2	Length 62
Best Local Similarity	50.0%	Pred. No. 5.6e-13		
Matches 28	Conservative 7	Mismatches 21	Indels 0	Gaps 0

```
Qy      2  EVRLLEPPTGPPCKARIIRMYFVASVGGCCNRRVYGGCGGNANNPASSEQECMSSCCG 57
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db      4  PKCHLPPKPGPCRAIIRFYNNPHSKQCEKFIYGGCHGNANKFKTIPDECNVYTCLG 59
```

RESULT 14
TITTOR

basic:Proteinase_inhibitor_logginead
CISpecies: Caretta caretta (10gginead)
CDate: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
CAccession: A01224
R:Kato, I.; Tomiura, N.
Fed. Proc. 38, 832, 1979
A>Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tandem
A:Reference number: A01224

Query Match	49.5%	Score 163	DB 1	length 110
Best Local Similarity	48.1%	Pred. No. 9.5e-13		
Matches	25	Conservative	16	Indels 0
				Gaps 0

Qy 5 CLLPATGPPCARIRIMYFVASVGQCNRFYVGCGCRGNANNFASDECMSSCQ 56

Db 8 CRLPBEGQPCGRIPIRYFYNPASRMCSFYGGCKGNKNFKTKALKECVRACR 59

RESULT 15

hypothetical protein R12A1.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #ext_change 09-Jul-2004
C:Accession: J32060
R:Pauley, A., Andrews, S.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid R12A1.
A:Reference number: Z21118
A:Accession: J32060
A:Stature: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-249 <PAU>
A:Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:AA66164.1; GSPDB:GN00023; CESP:f
C:Experimental source: strain Bristol N2; clone R12A1
C:Genetics:
A:Gene: CESP:R12A1.3
A:Map position: 5
A:introns: 75/1, 139/1

Query Match	48.9%	Score 161;	DB 2;	Length 249;
Best Local Similarity	55.6%	Pred. No. 3.5e-12;		
Matches 30; Conservative	8;	Mismatches 12;	Indels 4;	Gaps 1.

```
Qy      5 CLIPATGPKARIIRWYFVASVGQCNRFYGGCGNANNFASGEQCMSSCGGS 58
      |||||:::||:::||:::||:::||:::||:::||:::||:::||:
Db      143 CSLPLAVGSGTAPAVFYDYDASSGRGNQNFYSGCGGNANFQS----LSSQGT 192
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Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:48:53 ; Search time 25 Seconds
(without alignments)
173.186 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329
Sequence: 1 YPVRCILPPATGPKARIIR.....RGNNANFASBOECMSSCGS 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodaca/1/iaa/5A.COMB.pep: *
2: /cgn2_6/ptodaca/1/iaa/5B.COMB.pep: *
3: /cgn2_6/ptodaca/1/iaa/6A.COMB.pep: *
4: /cgn2_6/ptodaca/1/iaa/6B.COMB.pep: *
5: /cgn2_6/ptodaca/1/iaa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodaca/1/iaa/backflite1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	264	80.2	58	3	US-09-369-494-1
2	264	80.2	58	4	US-09-369-494-1
3	264	80.2	189	3	US-09-369-494-15
4	264	80.2	189	4	US-09-369-494-15
5	220.5	67.0	51	3	US-09-369-494-9
6	220.5	67.0	51	4	US-09-369-494-9
7	208	63.2	109	1	US-08-084-718-75
8	208	63.2	109	1	US-08-084-718-75
9	208	63.2	109	1	US-08-084-718-75
10	203	61.7	111	1	US-08-084-718-59
11	203	61.7	111	1	US-08-084-718-59
12	203	61.7	111	1	US-08-084-718-59
13	202	61.4	109	1	US-08-084-718-71
14	202	61.4	109	1	US-08-084-718-71
15	202	61.4	109	1	US-08-084-718-71
16	198	60.2	141	1	US-08-084-718-69
17	198	60.2	141	1	US-08-084-718-69
18	198	60.2	141	1	US-08-084-718-69
19	194	59.0	58	1	US-08-084-718-41
20	194	59.0	58	1	US-08-084-718-41
21	194	59.0	58	1	US-08-084-718-41
22	194	59.0	111	1	US-08-084-718-61
23	194	59.0	111	1	US-08-084-718-61
24	194	59.0	111	1	US-08-084-718-61
25	194	59.0	141	1	US-08-084-718-77
26	194	59.0	141	1	US-08-084-718-77
27	194	59.0	141	1	US-08-084-718-77

28	194	59.0	141	1	US-08-443-976-81	Sequence 81, Appl
29	194	59.0	141	1	US-08-443-977-77	Sequence 77, Appl
30	194	59.0	141	1	US-08-443-977-81	Sequence 81, Appl
31	193	58.7	56	1	US-07-598-737C-33	Sequence 33, Appl
32	193	58.7	56	1	US-08-084-718-34	Sequence 34, Appl
33	193	58.7	56	1	US-08-443-976-34	Sequence 34, Appl
34	193	58.7	56	1	US-08-443-977-34	Sequence 34, Appl
35	193	58.7	57	4	US-08-896-322-5	Sequence 5, Appl1
36	193	58.7	141	1	US-08-084-718-65	Sequence 65, Appl
37	193	58.7	141	1	US-08-084-718-73	Sequence 73, Appl
38	193	58.7	141	1	US-08-443-976-65	Sequence 65, Appl
39	193	58.7	141	1	US-08-443-976-73	Sequence 73, Appl
40	193	58.7	141	1	US-08-443-977-65	Sequence 65, Appl
41	193	58.7	141	1	US-08-443-977-73	Sequence 73, Appl
42	192	58.4	58	1	US-07-664-989B-44	Sequence 44, Appl
43	192	58.4	58	1	US-07-598-737C-1	Sequence 1, Appl1
44	192	58.4	58	1	US-08-084-718-1	Sequence 1, Appl1
45	192	58.4	58	1	US-08-084-718-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1		US-09-369-494-1	US-09369494
Sequence 1, Application		US-09369494	
Patent No. 6180607			
GENERAL INFORMATION:			
APPLICANT: Davies, Christopher			
APPLICANT: Chen, Dadong			
TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity			
FILE REFERENCE: MSB-7260			
CURRENT FILING DATE: 1999-08-05			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: Patentin Ver. 2.0			
SEQ ID NO 1			
LENGTH: 58			
TYPE: PRT			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: fragment from			
US-09-369-494-1			
Query Match		80.2%;	Score 264; DB 3; Length 58;
Best Local Similarity		82.8%;	Pred. No. 1.7e-25;
Matches 48; Conservative		0; Mismatches 10; Indels 0; Gaps 0;	
QY		1 YPVRCILPPATGPKARIIRWVAVSGCGRFVYGGCGNNANFASBOECMSSCGS 58	
DB		1 YPVRCILPPATGPKARIIRWVAVSGCGRFVYGGCGNNANFASBOECMSSCGS 58	
RESULT 2		US-09-569-670-1	US-09569670
Sequence 1, Application		US-09569670	
Patent No. 6689582			
GENERAL INFORMATION:			
APPLICANT: Davies, Christopher			
APPLICANT: Chen, Dadong			
APPLICANT: Rocznik, Steve			
TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity			
FILE REFERENCE: MSB-7260			
CURRENT FILING DATE: 2000-05-12			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: Patentin Ver. 2.0			
SEQ ID NO 1			
LENGTH: 58			
TYPE: PRT			
ORGANISM: Artificial Sequence			

binding site

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-1
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```
Query Match      80.2%; Score 264; DB 4; Length 58;
Best Local Similarity 82.8%; Pred. No. 1.7e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY      1 YPVRCLLPPTGPKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCOGS 58
Db      1 YPVRCLLPASHGSCADWAARWYFVASVGQCNRFWYGCGCHGNANNFASBOECMSSCOGS 58
```

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RESULT 3
US-09-369-494-15
; Sequence 15, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-15
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```
Query Match      80.2%; Score 264; DB 3; Length 189;
Best Local Similarity 82.8%; Pred. No. 5.9e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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```
QY      1 YPVRCLLPPTGPKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCOGS 58
Db      10 YPVRCLLPASHGSCADWAARWYFVASVGQCNRFWYGCGCHGNANNFASBOECMSSCOGS 67
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```
RESULT 4
US-09-569-670-15
; Sequence 15, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-15
```

```
Query Match      80.2%; Score 264; DB 4; Length 189;
Best Local Similarity 82.8%; Pred. No. 5.9e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY      1 YPVRCLLPPTGPKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCOGS 58
Db      10 YPVRCLLPASHGSCADWAARWYFVASVGQCNRFWYGCGCHGNANNFASBOECMSSCOGS 67
```

```
RESULT 5
US-09-369-494-9
; Sequence 9, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-9
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Query Match      67.0%; Score 220.5; DB 3; Length 51;
Best Local Similarity 80.8%; Pred. No. 3.4e-20;
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
```

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QY      5 CILPPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCO 56
Db      1 CILPPASHGSCADWAARWYFVASVGQCNRFWYGCG-GNANNFASBOECMSSCO 51
```

```
RESULT 6
US-09-569-670-9
; Sequence 9, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-9
```

```
Query Match      67.0%; Score 220.5; DB 4; Length 51;
Best Local Similarity 80.8%; Pred. No. 3.4e-20;
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
```

```
QY      5 CILPPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCO 56
Db      1 CILPPASHGSCADWAARWYFVASVGQCNRFWYGCG-GNANNFASBOECMSSCO 51
```

```
RESULT 7
US-08-084-718-75
; Sequence 75, Application US/08084718
; Patent No. 5591603
```

GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5591603xis, Kjeld
APPLICANT: Diness, Viggo
APPLICANT: No. 5591603xskov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5591603xis, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5591603o No. 5591603disk of No. 5591603th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,718
FILING DATE: 19930623
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143, 224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-084-718-75
Query Match 63.2%; Score 208; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 2.6e-18;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
Qy 5 CLLPATGPKARIIRMYFVAVGQCNRPYGGCGRNANFASBOCMSCGGS 58
Db 56 CLPPTGPKARIIRYFNKAGLQCTFYGGCGRNANFASBOCMETCGA 109
RESULT 8
US-08-443-976-75
Sequence 75, Application US/08443976
Patent No. 5618915
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5618915xis, Kjeld
APPLICANT: Diness, Viggo
APPLICANT: No. 5618915xskov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5618915xis, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5618915o No. 5618915disk of No. 5618915th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,976
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-976-75

Query Match 63.2%; Score 208; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 2.6e-18;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLPPTGPKARIIRYFVASVGCNRPYVGGCGGNANFASBQECMSSCGS 58
Db 56 CLEPSTGPKARIIRYFNAKAGLCQTFVYGGCGRGNNGNFKSABDQMETCGA 109

RESULT 9
US-08-443-977-75
Sequence 75, Application US/08443977
Patent No. 5621074
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5621074r1s, Kjeld
APPLICANT: Dinesb, Viggo
APPLICANT: No. 5621074rskov-Lauritsen, Lelf
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5621074r1s, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5621074d No. 5621074disk of No. 5621074th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,977
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4561,87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-977-75

Query Match 63.2%; Score 208; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 2.6e-18;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLPPTGPKARIIRYFVASVGCNRPYVGGCGGNANFASBQECMSSCGS 58
Db 56 CLEPSTGPKARIIRYFNAKAGLCQTFVYGGCGRGNNGNFKSABDQMETCGA 109

RESULT 10
US-08-084-718-59
Sequence 59, Application US/08084718
Patent No. 5591603
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5591603r1s, Kjeld
APPLICANT: Dinesb, Viggo
APPLICANT: No. 5591603rskov-Lauritsen, Lelf
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5591603r1s, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5591603d No. 5591603disk of No. 5591603th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Query Match 61.7%; Score 203; DB 1; Length 111;
Best Local Similarity 59.6%; Pred. No. 1,1e-17;
Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 PVRCLLPPTGPKARIRIRWYFVASVGCNRFYVGGCRGNANFPASQECMSSCGS 58
DB 55 PDCLEPPESTGPKARIRIRFYDATAGLCTETFYVGGCRANRNNFKSABDCMETCGGA 111

RESULT 12
US-08-443-977-59
Sequence 59, Application US/08443977
Patent No. 5621074
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5621074xis, Kjeld
APPLICANT: Dinesen, Viggo
APPLICANT: No. 5621074rekov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5621074xis, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56210740 No. 5621074disk of No. 5621074th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,977
CLASSIFICATION: 530
FILING DATE: 18-MAY-1995
APPLICATION NUMBER: US 08/084,718
PRIOR APPLICATION DATA:
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-977-59

Query Match 61.7%; Score 203; DB 1; Length 111;
Best Local Similarity 59.6%; Pred. No. 1,1e-17;
Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 PVRCLLPPTGPKARIRIRWYFVASVGCNRFYVGGCRGNANFPASQECMSSCGS 58
DB 55 PDCLEPPESTGPKARIRIRFYDATAGLCTETFYVGGCRANRNNFKSABDCMETCGGA 111

RESULT 13
US-08-084-718-71
Sequence 71, Application US/08084718
Patent No. 5591603
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5591603xis, Kjeld
APPLICANT: Dinesen, Viggo
APPLICANT: No. 5591603rekov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5591603xis, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55916030 No. 5591603disk of No. 5591603th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,718
CLASSIFICATION: 514
FILING DATE: 19930623
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408

FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143,224-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-084-718-71

Query Match 61.4%; Score 202; DB 1; Length 109;
Best Local Similarity 61.1%; Pred. No. 1,4e-17;
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLLPATGPKKARIIRYFVASVGCNRFYVGGCGRGNANNPASBOECMSSCGGS 58
Db 56 CLPSTGPKKARIIRYFVDATGICETFYVGGCRANRNPFKSAEDCMETCGGA 109

RESULT 14
US-08-443-976-71
Sequence 71, Application US/08443976
Patent No. 5618915
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5618915ris, Kjeld
APPLICANT: Diness, Viggo
APPLICANT: No. 5618915rbkov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Brengsaard, Claus
APPLICANT: No. 5618915ris, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 56189150 No. 5618915disk of No. 5618915th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,976

FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-976-71

Query Match 61.4%; Score 202; DB 1; Length 109;
Best Local Similarity 61.1%; Pred. No. 1,4e-17;
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLLPATGPKKARIIRYFVASVGCNRFYVGGCGRGNANNPASBOECMSSCGGS 58
Db 56 CLPSTGPKKARIIRYFVDATGICETFYVGGCRANRNPFKSAEDCMETCGGA 109

RESULT 15
US-08-443-977-71
Sequence 71, Application US/08443977
Patent No. 5621074
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5621074ris, Kjeld
APPLICANT: Diness, Viggo
APPLICANT: No. 5621074rbkov-Lauritsen, Leif
APPLICANT: Christensen, Niels D.
APPLICANT: Brengsaard, Claus
APPLICANT: No. 5621074ris, Fanny

APPLICANT: Peteren, Lars C.
 TITLE OF INVENTION: Process for the Preparation of Aprotinin
 TITLE OF INVENTION: and Aprotinin Analogs
 NUMBER OF SEQUENCES: 83
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 56210740 No. 5621074disk of No. 5621074th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,977
 FILING DATE: 18-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/084,718
 FILING DATE: 23-JUN-1993
 APPLICATION NUMBER: DK 4501/87
 FILING DATE: 28-AUG-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2254/88
 FILING DATE: 26-APR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK89/00096
 FILING DATE: 25-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/466,408
 FILING DATE: 21-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2361/90
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/598,337
 FILING DATE: 19-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 1118/91
 FILING DATE: 12-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00299
 FILING DATE: 01-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,687
 FILING DATE: 29-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/024,925
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Agtis, Cheryl H.
 REGISTRATION NUMBER: 34,086
 REFERENCE/DOCKET NUMBER: 3143.224-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-443-977-71

Query Match 61.4%; Score 202; DB 1; Length 109;
 Best Local Similarity 61.1%; Pred. No. 1,4e-17;
 Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CILPRTGCKARIRIRYFVSVGQNRFYVGGCGRNNANFASBQECMSSCCGS 58
 Db 56 CLEPSTGCKARIRIRYFVDATAGLCETFYVGGCRANRNNFASBQECMSSCCGA 109
 Search completed: August 25, 2005, 04:56:24
 Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:45:06 ; Search time 176 Seconds
(without alignments)
168.753 Million cell updates/sec

Title: US-10-721-961-4
Perfect score: 329
Sequence: 1 YPVRCLLPATGPCKARIR.....RGNANFPASGEQCMSSCGQS 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	80.2	531	2	Q659F2
2	264	80.2	531	2	Q6ZNM1
3	264	80.2	531	2	Q7Z681
4	264	80.2	531	2	Q95428
5	264	80.2	531	2	Q95428
6	192	58.4	100	1	BPT1_BOVIN
7	192	58.4	100	1	BPT1_BOVIN
8	188	57.1	58	2	Q7M311
9	186	56.5	984	2	Q9GON1
10	186	56.5	984	2	Q9GON2
11	185	56.2	327	2	Q6IND9
12	184	55.9	60	1	IBPS_BOVIN
13	184	55.9	100	1	BPT2_BOVIN
14	177	53.8	82	2	Q7Z2T3
15	174	52.9	122	1	UPT1_PIG
16	172	52.3	80	2	Q8T357
17	168	51.1	111	2	Q7M4L3
18	168	51.1	523	2	Q14594
19	168	51.1	738	2	Q90W28
20	168	51.1	738	2	Q6NUZ1
21	168	51.1	751	2	Q60709
22	168	51.1	753	1	APP2_HUMAN
23	168	51.1	753	2	Q7I1U0
24	168	51.1	753	2	Q6I482
25	168	51.1	753	2	APP2_RAT
26	166	50.5	283	1	Q6ZNT4
27	166	50.5	576	2	Q8TEU8
28	166	50.5	576	2	Q6UXZ9
29	165	50.2	82	2	Q8MVB4
30	165	50.2	83	2	Q90WA0
31	165	50.2	252	1	SPT2_HUMAN

32	165	50.2	252	2	Q6LEU8	Q6LEU8 homo sapien
33	164	49.8	61	1	IVB1_VIPAA	P00991 vipera ammo
34	164	49.8	90	2	Q6XPY8	Q6XPY8 vipera ammo
35	163	49.5	57	2	Q7M4I1	Q7M4I1 lymnaea sta
36	163	49.5	62	1	IVBT_OXYSC	Q7I24 oxyurans s
37	163	49.5	110	1	IBP_CARCR	P00993 caretta car
38	163	49.5	193	2	Q6P796	Q6P796 rattus norv
39	163	49.5	571	2	Q7TON3	Q7TON3 mus muscula
40	162	49.2	58	1	AXPI_ANTAF	P81547 anthopleura
41	162	49.2	58	1	Q9TW99	Q9TW99 anemone su
42	162	49.2	83	2	Q90W98	Q90W98 pseudonaja
43	161	48.9	133	2	Q8HZ45	Q8HZ45 papio papio
44	161	48.9	253	2	Q16701	Q16701 caenorhabd
45	161	48.9	751	2	Q9DCJ7	Q9DCJ7 gallus gall

ALIGNMENTS

RESULT 1	ID	Q659F2	PRELIMINARY;	PRT;	531 AA.
AC	Q659F2				
DT	25-OCT-2004	(T-EMBLrel. 28, Created)			
DT	25-OCT-2004	(T-EMBLrel. 28, Last sequence update)			
DE	25-OCT-2004	(T-EMBLrel. 28, Last annotation update)			
GN	Hypothetical protein DKFZp434F053	(Fragment).			
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RG	The German CDNA Consortium;				
RA	Wambolt R., Heubner D., Mewes H.W., Weil B., Amid C., Osaenger A.,				
RA	Fobo G., Han M., Wiemann S.;				
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AL10280; CAH56406.1; -.				
KW	Hypothetical protein.				
FT	NON TER				
FT	SEQUENCE 531 AA; 57158 MW; FEEDBC662369027B CRC64;				
Query Match		80.2%;	Score 264;	DB 2;	Length 531;
Best Local Similarity		82.8%;	Pred. No. 2.5e-23;		
Matches	48;	Conservative	0;	Mismatches	10;
				Indels	0;
				Gaps	0;
Qy	1 YPVRCLLPATGPCKARIRWYFASVGGQCNRPVYGGCGGNANFPASGEQCMSSCGQS 58				
Db	2 YPVRCLLPATGPCKARIRWYFASVGGQCNRPVYGGCGGNANFPASGEQCMSSCGQS 59				
RESULT 2					
Q6ZNM1					
AC	Q6ZNM1				
DT	05-JUL-2004	(T-EMBLrel. 27, Created)			
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)			
DE	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)			
GN	FLJ00259 protein (Fragment).				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Spleen;				
RA	Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.				
DR	EMBL: AK131073; BAC85123.1; -.				

DR HSSP: 016019; 1AAP.
 DR GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00406; IGV; 3.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS50900; PLAC; 1.
 DR NON_TER 1
 FT SEQUENCE 659 AA; 70274 MW; 50FFA993BB44C092 CRC64;

Query Match 80.2%; Score 264; DB 2; Length 659;
 Best Local Similarity 82.8%; Pred. No. 3, 1e-23;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIWFVSVGQCNRFFVYGGCGRGNANNFASDEQCMSSCGGS 58
 DB 131 YPVRCILPPAHGSCADMAARWYFVASVGCNRFWYGCGHGNANNFASDEQCMSSCGGS 188

RESULT 3
 ID Q72681 PRELIMINARY; PRT; 660 AA.
 AC Q72681;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp79D0163 (Fragment).
 GN Name=DKFZp79D0163;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
 RA Fobo G., Han M., Wiemann S.,
 RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; BX53757; CAD97826.1; -.
 DR HSSP; Q16019; 1AAP.
 DR GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS50900; PLAC; 1.
 DR Hypothetical protein.
 KW NON_TER 1
 FT SEQUENCE 660 AA; 70374 MW; A6D5B1C50CBB8015 CRC64;

Query Match 80.2%; Score 264; DB 2; Length 660;
 Best Local Similarity 82.8%; Pred. No. 3, 1e-23;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIWFVSVGQCNRFFVYGGCGRGNANNFASDEQCMSSCGGS 58
 DB 132 YPVRCILPPAHGSCADMAARWYFVASVGCNRFWYGCGHGNANNFASDEQCMSSCGGS 189

RESULT 4

ID 095428 PRELIMINARY; PRT; 1235 AA.
 AC 095428;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
 RA Madan A., Dickhoff R., Shaffer T., James R., Lesky S., Hood L.,
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AF109907; AAC97963.1; -.
 DR HSSP; P1211; 1KTH.
 DR Genew; HGNC:15262; PAPLN.
 DR GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR010294; ADMN_spacer1; 1.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF05986; ADMN_spacer1; 1.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00090; TSP 1; 5.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00209; TSP1; 5.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS50900; PLAC; 1.
 DR PROSITE; PS50902; TSP1; 5.
 DR Hypothetical protein.
 KW Name=Papln;
 GN Name=Papln;
 OS Mus musculus (Mouse).

Query Match 80.2%; Score 264; DB 2; Length 1235;
 Best Local Similarity 82.8%; Pred. No. 5, 6e-23;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIWFVSVGQCNRFFVYGGCGRGNANNFASDEQCMSSCGGS 58
 DB 688 YPVRCILPPAHGSCADMAARWYFVASVGCNRFWYGCGHGNANNFASDEQCMSSCGGS 745

RESULT 5

ID 09EPX2 PRELIMINARY; PRT; 1280 AA.
 AC 09EPX2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Papilin.
 GN Name=Papln;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1;
 RX MEDLINE=20530499; Pubmed=11076767;
 RA Kramerova I.A., Kawaguchi N., Nelson R.B., Fessler L.I., Chen Y.,
 RA Stieron A.L., Prockop D.J., Fessler J.H., Ackley B.D.,
 RT "Papilin in development, a pericellular protein with a homology to the
 RT ADAMTS metalloproteinases.";
 RL Development 127:5475-5485(2000).
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP: PL111; 1KTH.
 DR MSD; MG12386139; Papln.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR010294; ADAM spacer1.
 DR InterPro: IPR001083; Decarboxylase2.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG C2.
 DR InterPro: IPR010909; PLAC.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR InterPro: IPR000884; TSPI.
 DR Pfam: PF05986; ADAM spacer1; 1.
 DR Pfam: PF00047; IG; 1.
 DR Pfam: PF00014; Kunitz; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00209; TSPI; 5.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00879; ODR_DC_2_2; UNKNOWN_1.
 DR PROSITE; PS50900; PLAC; 1.
 DR PROSITE; PS50092; TSPI; 5.
 SQ SEQUENCE 1280 AA; 138823 MW; AE287705E61AF30 CRC64;
 SO
 Query Match 74.8%; Score 246; DB 2; Length 1280;
 Best Local Similarity 75.4%; Pred. No. 8.5e-21;
 Matches 43; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 YPVRCILPPTATGPGCKARIIMFYASVGCNRRFYGGCGNANNFASGEQCMSSCG 57
 DB 746 YPVRCILPSPAGSGCGDWARWYFVASVGRCNRFYGGCGNANNFASGEQCMNTCRG 802
 RESULT 6
 BPTI_BOVIN STANDARD; PRT; 100 AA.
 ID BPTI_BOVIN
 AC P00974;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Pancreatic trypsin inhibitor precursor (Basic protease inhibitor)
 DE (BPTI) (BPTI) (aprotinin).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87283904; Pubmed=2441071;
 RA Creighton T.E., Charles I.G.;
 RT "Sequences of the genes and polypeptide precursors for two bovine
 RT protease inhibitors.";
 RL J. Mol. Biol. 194:11-22(1987).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88295740; Pubmed=2456884;
 RA Creighton T.E., Charles I.G.;
 RT "Biosynthesis, processing, and evolution of bovine pancreatic trypsin
 RT inhibitor.";
 RL Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).
 RN [3]
 RP SEQUENCE OF 34-97 FROM N.A.
 RX MEDLINE=86158754; Pubmed=2420326;
 RA Kingston I.B., Anderson S.;
 RT "Sequences encoding two trypsin inhibitors occur in strikingly similar
 RT genomic environments.";
 RL Biochem. J. 233:443-450(1986).
 RN [4]
 RP SEQUENCE OF 34-97 FROM N.A.
 RX MEDLINE=84070725; Pubmed=6580617;
 RA Anderson S., Kingston I.B.;
 RT "Isolation of a genomic clone for bovine pancreatic trypsin inhibitor
 RT by using a unique-sequence synthetic DNA probe.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6838-6842(1983).
 RN [5]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66083012; Pubmed=5860161;
 RA Kassel B., Laekowski M.;
 RT "The basic trypsin inhibitor of bovine pancreas. V. The disulfide
 RT linkages.";
 RL Biochem. Biophys. Res. Commun. 20:463-468(1965).
 RN [6]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66171231; Pubmed=5296424;
 RA Anderer F.A., Horne S.;
 RT "The disulfide linkages in kallikrein inactivator of bovine lung.";
 RL J. Biol. Chem. 241:1568-1572(1966).
 RN [7]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=68012003; Pubmed=6053284;
 RA Chauvet J., Acher R.;
 RT "Covalent structure of a polypeptide inhibitor of trypsin (Kunitz and
 RT Northrop inhibitor).";
 RL Bull. Soc. Chim. Biol. 49:985-1000(1967).
 RN [8]
 RP SEQUENCE OF 36-93.
 RA Dlouha V., Pospisilova D., Meloun B., Sorm F.;
 RT "Sequence of residues 18-20 in pancreatic trypsin inhibitor.";
 RL Collect. Czech. Chem. Commun. 33:1363-1365(1968).
 RN [9]
 RP SEQUENCE OF 36-81.
 RC TISSUE=Adrenal chromaffin;
 RX MEDLINE=90211226; Pubmed=2322242;
 RA Lewis R.V., Ray P., Coghill R., Kruggel W.;
 RT "Presence of pancreatic trypsin inhibitor in adrenal medullary
 RT chromaffin cells.";
 RL Biochem. Biophys. Res. Commun. 167:543-547(1990).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA Deisenhofer J., Steigemann W.;
 RT "Crystallographic refinement of the structure of bovine pancreatic
 RT trypsin inhibitor at 1.5-A resolution.";
 RL Acta Crystallogr. B 31:238-250(1975).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=70255230; Pubmed=5447861;
 RA Huber R., Kukla D., Ruhlmann A., Epp O., Formanek H.;
 RT "The basic trypsin inhibitor of bovine pancreas. I. Structure analysis
 RT and conformation of the polypeptide chain.";
 RL Naturwissenschaften 57:389-392(1970).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.
 RX MEDLINE=91332906; Pubmed=1714504;
 RA Housset D., Kim K.-S., Fuchs J., Woodward C., Wlodawer A.;
 RT "Crystal structure of a Y35G mutant of bovine pancreatic trypsin
 RT inhibitor.";
 RL J. Mol. Biol. 220:757-770(1991).

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 59 AA; 6591 MW; B963C93192BB4418 CRC64;
Query Match 57.8%; Score 190; DB 2; Length 59;
Best Local Similarity 56.1%; Pred. No. 2.3e-15; Indels 0; Gaps 0;
Matches 32; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
QY 2 PVRCLEPPATGPKARIRMYFVASVGQCNRFYVGGCGGNANFPASEQECSSCGGS 58
3 PDFCLBPPYGPCKAMIRYFYNAKGLCCPFYVGGCGRAKNNFKSAEDCMRTCCGA 59
ID Q7M312 PRELIMINARY; PRT; 58 AA.
AC Q7M312;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Isoaprotinin G2.
OS Bos indicus x Bos taurus (hybrid cattle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=30522;
OX [1]
RN [1]
RX MEDLINE=88221840; Pubmed=2453200;
RA Stekemann J., Wenzel H.R., Schroeder W., Tescheche H.;
RT "Characterization and sequence determination of six aprotonin
RT homologues from bovine lungs."
RL Biol. Chem. Hoppe-Seyler 369:157-163 (1988).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P00974; 1BPT.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot. Inh. Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot. Inh. Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 58 AA; 6532 MW; B858E6092EA1518 CRC64;
Query Match 57.1%; Score 188; DB 2; Length 58;
Best Local Similarity 56.1%; Pred. No. 4e-15; Indels 0; Gaps 0;
Matches 32; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 2 PVRCLEPPATGPKARIRMYFVASVGQCNRFYVGGCGGNANFPASEQECSSCGGS 58
3 PDFCLBPPYGPCKAMIRYFYNAKGLCCPFYVGGCGRAKNNFKSAEDCMRTCCGA 58
ID Q9G0N1 PRELIMINARY; PRT; 984 AA.
AC Q9G0N1;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliacis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynarthae; Hormathidae; Calliacis.
OC NCBI_TaxID=6114;
OX [1]
RN [1]
RX SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221986; AAG44251.1; -.
DR HSSP; P12111; 1KNT.

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; F:peptide metabolism; IEA.
DR InterPro; IPR011044; Amino DH B-like.
DR InterPro; IPR001258; NTL.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR000720; Pamonoxgenase.
DR InterPro; IPR008977; PHM_PNGase_F.
DR InterPro; IPR002223; Prot. Inh. Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NTL; 5.
DR PRINTS; PR00759; BASICTPASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110265 MW; 4C24E4BCB3B480D CRC64;
Query Match 56.5%; Score 186; DB 2; Length 984;
Best Local Similarity 54.5%; Pred. No. 1.1e-13;
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 1 YPVRCLEPPATGPKARIRMYFVASVGQCNRFYVGGCGGNANFPASEQECSSC 55
726 FPAFCMLBHDTPCRAAMPYFADAKARSCTRFYVGGCGGNENFPASKRECEAKC 780
ID Q9G0N2 PRELIMINARY; PRT; 984 AA.
AC Q9G0N2;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliacis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynarthae; Hormathidae; Calliacis.
OC NCBI_TaxID=6114;
OX [1]
RN [1]
RX SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; F:peptide metabolism; IEA.
DR InterPro; IPR011044; Amino DH B-like.
DR InterPro; IPR001258; NTL.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR000720; Pamonoxgenase.
DR InterPro; IPR008977; PHM_PNGase_F.
DR InterPro; IPR002223; Prot. Inh. Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NTL; 5.
DR PRINTS; PR00759; BASICTPASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR ProDom; PD000222; Prot. Inh. Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE: PSS0279; BPTI_KUNITZ_2; 1.
DR PROSITE: PSS0084; CU2_MONOOXYGENASE_1; 1.
DR MONOOXYGENASE.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78EBC CRC64;

Query Match
Best Local Similarity 54.5%; Score 186; DB 2; Length 984;
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANPFASBECMSSSC 55
Db 726 PFAFCILBHDTGCRAMPFRWYFDAKARSCRTIRYGGCGGNENPFASKECEKAC 780

RESULT 11
O6IND9 PRELIMINARY; PRT; 327 AA.
AC O6IND9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MGCB165 protein (Fragment).
GN Name=MGCB165;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Uedini T.B., Tomihata S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL: BC072344; AAH72344.1; -.
DR HSSP: Q16019; IAP.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0030414; F:protease inhibitor activity; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0007596; P:blood coagulation; IEA.

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DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR InterPro: IPR008296; TPPI.
DR Pfam: PF0014; Kunitz_BPTI; 3.
DR PIRSF: PIRSF001620; TPPI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 3.
DR SMART: SM00131; KU; 3.
DR PROSITE: PSS0280; BPTI_KUNITZ_1; 2.
DR PROSITE: PSS0279; BPTI_KUNITZ_2; 3.
FT NON TER 1
SQ SEQUENCE 327 AA; 35951 MW; 2BFE6FA75DAB0497 CRC64;

Query Match
Best Local Similarity 56.2%; Score 185; DB 2; Length 327;
Matches 29; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANPFASBECMSSSCG 57
Db 197 YSEYCABSLTPGCAHSFRWYDRTTSGCATFYGGCGGNANVLSDDCVKNCVG 253

RESULT 12
IBPS_BOVIN STANDARD; PRT; 60 AA.
ID IBPS_BOVIN
AC P00975;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum basic protease inhibitor (Serum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxId=9913;
[1]
RP SEQUENCE.
RX MEDLINE=81044408; PubMed=7428928; DOI=10.1016/0014-5793(80)80997-5;
RA Wachter E., Deppner K., Hochstrasser K., Lempert K., Geiger R.;
RT "A new Kunitz-type inhibitor from bovine serum amino acid sequence
RT determination."
RL FEBS Lett. 119:58-62(1980).
CC -1- FUNCTION: This inhibitor has activity very similar to that of the
CC -1- basic protease inhibitor from bovine tissues.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: A01206; TIBOR.
DR HSSP: P00974; IBPI.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PSS0280; BPTI_KUNITZ_1; 1.
DR PROSITE: PSS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 17 18
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT DISULFID 32 53
SQ SEQUENCE 60 AA; 6647 MW; B9953EBAACF1A4E6 CRC64;

Query Match
Best Local Similarity 55.9%; Score 184; DB 1; Length 60;
Matches 31; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

OY 2 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANPFASBECMSSSCG 58
Db 4 YDFCLPEPTGPKAMIRFYNAAGFCETFYGGCGAKSNFYSADCKRTCGA 60

RESULT 13
BPT2_BOVIN STANDARD; PRT; 100 AA.
ID BPT2_BOVIN

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AC P04815;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Spleen trypsin inhibitor I precursor (SI-I) [Contains: Spleen trypsin inhibitor II (SI-II); Spleen trypsin inhibitor III (SI-III)].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87283904; PubMed=2441071;
 RA Creighton T.E., Charles I.G.;
 RT "Sequences of the genes and polypeptide precursors for two bovine protease inhibitors";
 RL J. Mol. Biol. 194:11-22(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88295740; PubMed=2456884;
 RA Creighton T.E., Charles I.G.;
 RT "Biogenesis, processing, and evolution of bovine pancreatic trypsin inhibitor";
 RL Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).
 RN [3]
 RP SEQUENCE OF 34-97 FROM N.A.
 RX MEDLINE=86158754; PubMed=2420326;
 RA Kingston I.B., Anderson S.;
 RT "Sequences encoding two trypsin inhibitors occur in strikingly similar genomic environments";
 RL Biochem. J. 233:443-450(1986).
 RN [4]
 RP SEQUENCE OF 34-99.
 RX MEDLINE=89076531; PubMed=2462435;
 RA Fioretto E., Angeletti M., Fiorucci L., Barra D., Bossa F., Ascoli F.;
 RT "Aprotinin-like isoinhibitors in bovine organs";
 RL Biol. Chem. Hoppe-Seyler 369:37-42(1988).
 RN [5]
 RP SEQUENCE OF 34-99.
 RX MEDLINE=89076531; PubMed=2462435;
 RA Fioretto E., Angeletti M., Fiorucci L., Barra D., Bossa F., Ascoli F.;
 RT "Aprotinin-like isoinhibitors in bovine organs";
 RL Biol. Chem. Hoppe-Seyler 369:37-42(1988).
 RN [6]
 RP SEQUENCE OF 36-93.
 RX MEDLINE=86008178; PubMed=2413011;
 RA Fioretto E., Iacopino G., Angeletti M., Barra D., Bossa F., Ascoli F.;
 RT "Primary structure and antiproteolytic activity of a Kunitz-type inhibitor from bovine spleen";
 RL J. Biol. Chem. 260:11451-11455(1985).
 RN [7]
 RP SEQUENCE OF 36-97.
 RX MEDLINE=81098238; PubMed=1986787; DOI=10.1016/0167-4838(91)90231-N;
 RA Barra D., Fioretto E., Angeletti M., Maras B., Bossa F., Ascoli F.;
 RT "Intermediate isoinhibitors from bovine spleen: primary structure of an isoinhibitor in the processing of the precursor";
 RL Biochim. Biophys. Acta 1076:143-147(1991).
 RN [8]
 RP SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M20935; AAA51418.1; -
 DR EMBL; M20931; AAA51418.1; JOINED.
 DR EMBL; M20933; AAA51418.1; JOINED.
 DR EMBL; X05275; CAA28887.1; -
 DR EMBL; X06685; CAA29881.1; -
 DR EMBL; X03366; CAA27064.1; ALT_SEQ.
 DR EMBL; X03366; CAA27065.1; -
 DR PIR; S00274; TIBOSP.
 DR HSSP; P00974; 1BPI.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor; Signal.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 33
 FT CHAIN 34 99 Spleen trypsin inhibitor I.
 FT CHAIN 36 97 Spleen trypsin inhibitor III.
 FT CHAIN 36 93 Spleen trypsin inhibitor II.
 FT DOMAIN 40 90 BPTI/Kunitz inhibitor.
 FT SITE 50 51 Reactive bond (by similarity).
 FT DISULFID 40 90 By similarity.
 FT DISULFID 49 73 By similarity.
 FT DISULFID 65 86 By similarity.
 SQ SEQUENCE 100 AA; 10843 MW; 39069734B8ACF4E3 CRC64;

Query Match 55.9%; Score 184; DB 1; Length 100;
 Best Local Similarity 52.6%; Pred. No. 2,1e-14;
 Matches 30; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVRCILPPATGPKAIIRMYFVASVCCNRFYGGCGGNANFSEGCSSCOSS 58
 Db 37 PDLCEPPYTPGCKAMIRYFYNAKAGFETFYGGCKAKSNFRSABDCMRTCGGA 93

RESULT 14

ID Q7ZT3 PRELIMINARY; PRT; 82 AA.
 AC Q7ZT3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Amyloid protein b (Fragment).
 GN Name=apbb;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Brachyoptera; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; A6771744; AAP22956.1; -
 DR HSSP; Q16019; 1AAP.
 DR ZFIN; ZDB-GENE-020220-1; apbb.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8874 MW; 0723D4AC658B349 CRC64;

Query Match 53.8%; Score 177; DB 2; Length 82;

Best Local Similarity 53.7%; Pred. No. 1,2e-13;
Matches 29; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 5 CLLPATGPKARIIRMYFVASVGQCNRFYVGGCRGNANNFASBDECMSSCGS 58
DB 22 CWAPASGPGCHALPRMYFVAEKGRCASTFGGCGGNRNFFSEBECMAVCSS 75

RESULT 15
UPTI_PIG STANDARD; PRT; 122 AA.

AC 029100;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Uterine plasmin/trypsin inhibitor precursor (UPTI).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RP SEQUENCE FROM N.A., SEQUENCE OF 30-56, AND CHARACTERIZATION.
RC TISSUE=Conceptus membrane, and Uterus;
RX MEDLINE=95014140; PubMed=7929061;
RA Stallings-Mann M.L., Burke M.G., Trout W.E., Roberts R.M.;
RT "Purification, characterization, and cDNA cloning of a Kunitz-type
protease inhibitor secreted by the porcine uterus.";
J. Biol. Chem. 269:24090-24094(1994).

CC -1- FUNCTION: Inhibitor of plasmin and trypsin. Also has a weak
affinity for chymotrypsin. Could serve to neutralize the
activities of one or more serine proteinases generated by the
proliferating trophoblast during the formation of the noninvasive
placenta.

CC -1- TISSUE SPECIFICITY: Expressed only in the uterus and the
endometrium.

CC -1- DEVELOPMENTAL STAGE: Maximally expressed during pregnancy until
day 30 after which levels decrease significantly.

CC -1- INDUCTION: By progesterone.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC EMBL, LI4282; AAA62425.1; -.
DR PIR; A55115; A55115.

DR HSSP; P00974; 1K09.
DR InterPro; IPR002223; ProtInh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.

DR PRODOM; PD000222; ProtInh_Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor; Signal.
FT SIGNAL 1 20 Potential.

FT PROPEP 21 29
FT CHAIN 30 122 Uterine plasmin/trypsin inhibitor.

FT DOMAIN 38 88 BPTI/Kunitz inhibitor.

FT SITE 48 49 Reactive bond (By similarity).

FT DISULFID 38 88 By similarity.

FT DISULFID 47 71 By similarity.

FT DISULFID 63 84 By similarity.

FT CONFLICT 36 36 G -> A (in Ref. 1; AA sequence).

FT CONFLICT 48 48 S -> R (in Ref. 1; AA sequence).

FT CONFLICT 52 52 V -> I (in Ref. 1; AA sequence).

FT CONFLICT 54 54 Y -> V (in Ref. 1; AA sequence).

SEQUENCE 122 AA; 13109 MW; B9BEFB3A6FB76CEC CRC64;

Query Match 52.9%; Score 174; DB 1; Length 122;

Best Local Similarity 51.9%; Pred. No. 4e-13;
Matches 28; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 PYRCLLPATGPKARIIRMYFVASVGQCNRFYVGGCRGNANNFASBDECMSSC 55
DB 35 PGCRFPFYTGPCHAFVAFYFNATTTGLGQSFYVGGCRGKQNNFMDEKCHLHTC 88

Search completed: August 25, 2005, 04:55:26
Job time : 180 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:49:39 ; Search time 162 Seconds
(without alignments)
140.197 Million cell updates/sec

Title: US-10-721-961-4
Perfect score: 329
Sequence: 1 YPVRCILPPATGPKARIIR.....RGNNANFASBOECSSCGS 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /cgnt2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgnt2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
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21: /cgnt2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
22: /cgnt2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	58	16	US-10-721-961-4
2	326	99.1	58	16	US-10-721-961-5
3	314	95.4	58	16	US-10-721-961-7
4	314	95.4	58	16	US-10-721-961-34
5	291	88.4	58	16	US-10-721-961-6
6	291	88.4	58	16	US-10-721-961-33
7	264	80.2	58	16	US-10-721-961-1
8	264	80.2	58	16	US-10-721-961-32
9	264	80.2	1280	15	US-10-262-839-92
10	264	80.2	1311	14	US-10-103-377C-6
11	264	80.2	1311	16	US-10-391-364-91

12	246	74.8	1280	14	US-10-087-887-86	Sequence 86, Appl
13	193	58.7	57	8	US-08-896-322-5	Sequence 5, Appl
14	193	58.7	57	14	US-10-252-967-5	Sequence 5, Appl
15	192	58.4	58	9	US-09-234-874A-7	Sequence 7, Appl
16	192	58.4	58	9	US-09-234-874A-108	Sequence 108, App
17	192	58.4	58	9	US-09-030-619-173	Sequence 173, App
18	192	58.4	58	9	US-09-912-609-61	Sequence 61, Appl
19	192	58.4	58	9	US-09-113-244-2	Sequence 2, Appl
20	192	58.4	58	9	US-09-781-988-44	Sequence 44, Appl
21	192	58.4	58	10	US-09-234-873A-7	Sequence 7, Appl
22	192	58.4	58	10	US-09-234-873A-108	Sequence 108, App
23	192	58.4	58	10	US-09-788-006-55	Sequence 55, Appl
24	192	58.4	58	10	US-09-893-878-44	Sequence 44, Appl
25	192	58.4	58	10	US-09-974-026-24	Sequence 24, Appl
26	192	58.4	58	10	US-09-896-095-44	Sequence 44, Appl
27	192	58.4	58	10	US-09-896-095-144	Sequence 144, App
28	192	58.4	58	10	US-09-896-095-181	Sequence 181, App
29	192	58.4	58	14	US-10-076-604-7	Sequence 7, Appl
30	192	58.4	58	14	US-10-076-604-108	Sequence 108, App
31	192	58.4	58	14	US-10-167-351-38	Sequence 38, Appl
32	192	58.4	58	14	US-10-038-722-6	Sequence 6, Appl
33	192	58.4	58	14	US-10-038-722-87	Sequence 87, Appl
34	192	58.4	58	14	US-10-038-722-124	Sequence 124, App
35	192	58.4	58	15	US-10-277-232-173	Sequence 173, App
36	192	58.4	58	15	US-10-126-685-44	Sequence 44, Appl
37	192	58.4	58	15	US-10-115-134-1	Sequence 1, Appl
38	192	58.4	58	15	US-10-115-134-38	Sequence 38, Appl
39	192	58.4	58	15	US-10-277-233-173	Sequence 173, App
40	192	58.4	58	15	US-10-127-028-44	Sequence 44, Appl
41	192	58.4	58	15	US-10-360-101-205	Sequence 205, App
42	192	58.4	58	15	US-10-126-544-44	Sequence 44, Appl
43	192	58.4	58	15	US-10-456-986A-29	Sequence 29, Appl
44	192	58.4	58	15	US-10-456-981-23	Sequence 23, Appl
45	192	58.4	58	17	US-10-718-966-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-721-961-4
; Sequence 4, Application US/10721961
; Publication No. US20040152633A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Jorgensen, Mariame U
; APPLICANT: Susanne, Bang
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
; FILE REFERENCE: 6297.204-US
; CURRENT APPLICATION NUMBER: US/10721,961
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/303,180
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/DK02/00372
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-721-961-4

Query Match 100.0%; Score 329; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 58; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
1 YPVRCILPPATGPKARIIRFVASVGCCRRFVIGCGGNNANFASBOECSSCGS 58
|||||

Db 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58

RESULT 2

US-10-721-961-5
; Sequence 5, Application US/10721961
; Publication No. US20040152633A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Jorgensen, Marianne U
; APPLICANT: Susanne, Bang
; APPLICANT: Olesen, Ole H
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
; FILE REFERENCE: 6297.204-US
; CURRENT APPLICATION NUMBER: US/10/721,961
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/303,180
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/DK02/00372
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-961-5

Query Match 99.1%; Score 326; DB 16; Length 58;
Best Local Similarity 98.3%; Pred. No. 1.3e-31;
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58
Db 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58

RESULT 3

US-10-721-961-7
; Sequence 7, Application US/10721961
; Publication No. US20040152633A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Jorgensen, Marianne U
; APPLICANT: Susanne, Bang
; APPLICANT: Olesen, Ole H
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
; FILE REFERENCE: 6297.204-US
; CURRENT APPLICATION NUMBER: US/10/721,961
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/303,180
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/DK02/00372
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-961-7

Query Match 95.4%; Score 314; DB 16; Length 58;
Best Local Similarity 94.8%; Pred. No. 3.6e-30;
Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58

Db 1 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58

RESULT 4

US-10-721-961-34
; Sequence 34, Application US/10721961
; Publication No. US20040152633A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Jorgensen, Marianne U
; APPLICANT: Susanne, Bang
; APPLICANT: Olesen, Ole H
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
; FILE REFERENCE: 6297.204-US
; CURRENT APPLICATION NUMBER: US/10/721,961
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/303,180
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/DK02/00372
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Amino acid sequence of the 212L-HK118-2 fusion polypeptide
US-10-721-961-34

Query Match 95.4%; Score 314; DB 16; Length 111;
Best Local Similarity 94.8%; Pred. No. 6.6e-30;
Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 58
Db 54 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNFASBQECMSSCGGS 111

RESULT 5

US-10-721-961-6
; Sequence 6, Application US/10721961
; Publication No. US20040152633A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Jorgensen, Marianne U
; APPLICANT: Susanne, Bang
; APPLICANT: Olesen, Ole H
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
; FILE REFERENCE: 6297.204-US
; CURRENT APPLICATION NUMBER: US/10/721,961
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/303,180
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/DK02/00372
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-961-6

Query Match 88.4%; Score 291; DB 16; Length 58;
Best Local Similarity 89.7%; Pred. No. 2.1e-27;

Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 YPVRCLLPPATGCGKARIIRWYFVASVGQCNRFFVGGCGGNANNFASSEQECMSSCCGS 58
 DB 1 YPVRCLLPPATGCGKMAARWYFVASVGQCNRFFWYGCGCHGNANNFASSEQECMSSCCGS 58

RESULT 6
 US-10-721-961-33
 ; Sequence 33, Application US/10721961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
 ; FILE REFERENCE: 6297.204-US
 ; CURRENT APPLICATION NUMBER: US/10/721,961
 ; PRIOR FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/303,180
 ; PRIOR FILING DATE: 2001-07-05,
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; PRIOR FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 33
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of the 212L-HK18-1 fusion polypeptide
 US-10-721-961-33

Query Match 88.4%; Score 291; DB 16; Length 111;
 Best Local Similarity 89.7%; Pred. No. 3.8e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 YPVRCLLPPATGCGKARIIRWYFVASVGQCNRFFVGGCGGNANNFASSEQECMSSCCGS 58
 DB 54 YPVRCLLPPATGCGKMAARWYFVASVGQCNRFFWYGCGCHGNANNFASSEQECMSSCCGS 111

RESULT 7
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 ; Sequence 1, Application US/10721961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
 ; FILE REFERENCE: 6297.204-US
 ; CURRENT APPLICATION NUMBER: US/10/721,961
 ; PRIOR FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/303,180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; PRIOR FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 58
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:

; OTHER INFORMATION: Amino acid sequence of human wild type HK1-18
 US-10-721-961-1
 Query Match 80.2%; Score 264; DB 16; Length 58;
 Best Local Similarity 82.8%; Pred. No. 3.7e-24;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCLLPPATGCGKARIIRWYFVASVGQCNRFFVGGCGGNANNFASSEQECMSSCCGS 58
 DB 1 YPVRCLLPPATGCGKADWMAARWYFVASVGQCNRFFWYGCGCHGNANNFASSEQECMSSCCGS 58
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 US-10-721-961-32
 ; Sequence 32, Application US/10721961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides
 ; FILE REFERENCE: 6297.204-US
 ; CURRENT APPLICATION NUMBER: US/10/721,961
 ; PRIOR FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/303,180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; PRIOR FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 32
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of the 212L-HK18 fusion polypeptide
 US-10-721-961-32

Query Match 80.2%; Score 264; DB 16; Length 111;
 Best Local Similarity 82.8%; Pred. No. 6.8e-24;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCLLPPATGCGKARIIRWYFVASVGQCNRFFVGGCGGNANNFASSEQECMSSCCGS 58
 DB 54 YPVRCLLPPATGCGKADWMAARWYFVASVGQCNRFFWYGCGCHGNANNFASSEQECMSSCCGS 111
 RESULT 9
 US-10-262-839-92
 ; Sequence 92, Application US/10262839
 ; Publication No. US20040038877A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook, John
 ; APPLICANT: Anderson, David W.,
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Caterton, Elina
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Leach, Martin
 ; APPLICANT: Li, Li
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Patuturajan, Meera
 ; APPLICANT: Reiger, Daniel

```

; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Vose, Edward,
; APPLICANT: Zernhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 92
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-839-92

Query Match      80.2%; Score 264; DB 15; Length 1280;
Best Local Similarity 82.8%; Pred. No. 6,7e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YVRCLLPAPGTCARIRIRWYFVASVGQCNRFVYGGCGGNANNPASBOECMSSCGGS 58
Db      752 YVRCLLPSAHGSCADMARWTFVASVGQCNRFWYGCGHGNANNPASBOECMSSCGGS 809

RESULT 10
; US-10-103-377C-6
; Sequence 6, Application US/10103377C
; Publication No. US20030073098A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 65577, A Human Matrix
; FILE REFERENCE: MP101-049PIRM
; CURRENT APPLICATION NUMBER: US/10/103,377C
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/278,347
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1311
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-103-377C-6

Query Match      80.2%; Score 264; DB 14; Length 1311;
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; Best Local Similarity 82.8%; Pred. No. 6,8e-23;
; Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YVRCLLPAPGTCARIRIRWYFVASVGQCNRFVYGGCGGNANNPASBOECMSSCGGS 58
Db      732 YVRCLLPSAHGSCADMARWTFVASVGQCNRFWYGCGHGNANNPASBOECMSSCGGS 789

RESULT 11
; US-10-391-364-91
; Sequence 91, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Welch, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; FILE REFERENCE: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; FILE REFERENCE: MP103-019OMNIM
; CURRENT APPLICATION NUMBER: US/10/391,364
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 1311
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-391-364-91

Query Match      80.2%; Score 264; DB 16; Length 1311;
Best Local Similarity 82.8%; Pred. No. 6,8e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YVRCLLPAPGTCARIRIRWYFVASVGQCNRFVYGGCGGNANNPASBOECMSSCGGS 58
Db      722 YVRCLLPSAHGSCADMARWTFVASVGQCNRFWYGCGHGNANNPASBOECMSSCGGS 789

RESULT 12
; US-10-087-887-86
; Sequence 86, Application US/10087887
; Publication No. US20030198957A1
; GENERAL INFORMATION:
; APPLICANT: Rekuda, Ramesh
; APPLICANT: Conley, Pamela B.
; APPLICANT: Yang, Ruey-Bing
; APPLICANT: Hart, Matthew
```

APPLICANT: Tomlinson, James E.
 APPLICANT: Topper, James N.
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Leach, Martin D.
 APPLICANT: Zernhusen, Bryan D.
 APPLICANT: Komuves, Laszlo
 APPLICANT: Padigaru, Muralidhara
 TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-285
 CURRENT APPLICATION NUMBER: US/10/087,887
 CURRENT FILING DATE: 2002-03-01
 PRIOR APPLICATION NUMBER: 60/273,049
 PRIOR FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: 60/279,883
 PRIOR FILING DATE: 2001-03-29
 PRIOR APPLICATION NUMBER: 60/277,791
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/281,248
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/282,864
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 60/282,537
 PRIOR FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 60/282,867
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: CuiBaseqlist version 0.1
 SEQ ID NO: 86
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-087-887-86
 Query Match 74.8%; Score 246; DB 14; Length 1280;
 Best Local Similarity 75.4%; Pred. No. 9,8e-21;
 Matches 43; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 YPVRCILPPTGCKARIIRMYFVASVGQCNRFYGGCGRGNANFPASEQECMSSCOG 57
 DB 746 YPVRCILPPTGCKARIIRMYFVASVGQCNRFYGGCGRGNANFPASEQECMSSCOG 802
 RESULT 13
 US-08-896-322-5
 Sequence 5, Application US/08896322
 Publication No. US20020103334A1
 GENERAL INFORMATION:
 APPLICANT: Werner Schroeder, Soren Bjorn, Kjeld No. US20020103334A1,ris, Viggo Dinesen
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE
 STREET: 660 White Plains Road
 City: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-5144
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 OPERATING SYSTEM: DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/896,322
 FILING DATE: 17-JUL-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 196 29 982.9 (Germany)
 FILING DATE: 25-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33,141
 REFERENCE/DOCKET NUMBER: Bayer 9911-KGB

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 332-1700
 TELEFAX: (914) 332-1844
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 Amino acids
 TYPE: Amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: linear
 ORIGINAL SOURCE:
 ORGANISM: Aprotinin variant
 US-08-896-322-5
 Query Match 58.7%; Score 193; DB 8; Length 57;
 Best Local Similarity 57.4%; Pred. No. 1.2e-15;
 Matches 31; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 5 CLPPTATGCKARIIRMYFVASVGQCNRFYGGCGRGNANFPASEQECMSSCOGS 58
 DB 4 CLPPTATGCKARIIRMYFVASVGQCNRFYGGCGRGNANFPASEQECMSSCOGS 57
 RESULT 14
 US-10-252-967-5
 Sequence 5, Application US/10252967
 Publication No. US20030096752A1
 GENERAL INFORMATION:
 APPLICANT: Werner Schroeder, Soren Bjorn, Kjeld No. US20030096752A1,ris, Viggo Dine
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE
 STREET: 660 White Plains Road
 City: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-5144
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 OPERATING SYSTEM: DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/252,967
 FILING DATE: 23-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/896,322
 FILING DATE: 17-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33,141
 REFERENCE/DOCKET NUMBER: Bayer 9911-KGB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 332-1700
 TELEFAX: (914) 332-1844
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 Amino acids
 TYPE: Amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: linear
 ORIGINAL SOURCE:
 ORGANISM: Aprotinin variant
 US-10-252-967-5

Query Match 58.7%; Score 193; DB 14; Length 57;
Best Local Similarity 57.4%; Pred. No. 1.2e-15;
Matches 31; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 5 CLPPTGPKARIIRMYFVASVGGCNRFPYGGCRGNANFPASEQECMSSCGS 58
DB 4 CLPPTGPKARIIRMYFVASVGGCNRFPYGGCNRANFPKSAEDCMETCGA 57

RESULT 15

US-09-234-874A-7
; Sequence 7, Application US/09234874A
; Publication No. US2001002003A1
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Lesikar, David D.
; Damm, Deborah
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
; US-09-234-874A-7

Query Match 58.4%; Score 192; DB 9; Length 58;
Best Local Similarity 57.9%; Pred. No. 1.7e-15;
Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 PVRCCLIPATGPKARIIRMYFVASVGGCNRFPYGGCRGNANFPASEQECMSSCGS 58
DB 2 PDCLEPPYTGPKARIIRMYFNAKAGLCQTFYGGCRANFPKSAEDCMRTCGA 58

Search completed: August 25, 2005, 04:59:08
Job time : 164 secs

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